```
   1 GTGCGAAAGG CTGCCAGCAT GTCATCAGTG AGCCCCATCC AGATCCCCAG
  51 TCGCCTCCCG CTGCTGCTCA CCCACGAGGG CGTCCTGCTG CCCGGCTCCA
 101 CCATGCGCAC CAGCGTGGAC TCGGCCCACA ACCTGCAGCT GGTGCGGAGC
 151 CGCCTTCTGA AGGGCACGTC GCTGCAAAGC ACCATCCTGG GCGTCATCCC
 201 CAACACGCCT GACCCCGCCA GCGACGCGCA GGACCTGCCG CCGCTGCACA
 251 GGATTGGCAC AGCTGCACTG GCCGTTCAGG TTGTGGGCAG TAACTGGCCC
 301 AAGCCCCACT ACACTCTGTT GATTACAGGC CTATGCCGTT TCCAGATTGT
 351 ACAGGTCTTA AAAGAGAAGC CATATCCCAT TGCTGAAGTG GAGCAGTTGG
 401 ACCGACTTGA GGAGTTTCCC AACACCTGTA AAATGAGGGA GGAGCTAGGA
 451 GAACTATCAG AGCAGTTTTA CAAATATGCA GTACAATTGG TTGAAATGTT
 501 GGATATGTCT GTCCCTGCAG TTGCTAAATT GAGACGTCTT TTAGATAGTC
 551 TTCCAAGGGA AGCTTTACCA GACATCTTGA CATCAATTAT CCGAACAAGC
 601 AACAAAGAGA AACTCCAGAT TTTAGATGCT GTGAGCCTAG AGGAGCGGTT
 651 CAAGATGACT ATACCACTGC TTGTCAGACA AATTGAAGGC CTGAAATTGC
 701 TTCAAAAAAC CAGAAAACCC AAGCAAGATG ATGATAAGAG GGTTATAGCA
 751 ATACGCCCTA TTAGGAGAAT TACACATATC TCAGGTACTT TAGAAGATGA
 801 AGATGAAGAT GAAGATAATG ATGACATTGT CATGCTAGAG AAAAAAATAC
 851 GAACATCTAG TATGCCAGAG CAGGCCCATA AAGTCTGTGT CAAAGAGATA
 901 AAGAGACTCA AAAAAATGCC TCAGTCAATG CCAGAATATG CTCTGACTAG
 951 AAATTATTTG GAACTTATGG TAGAACTTCC TTGGAACAAA AGTACAACTG
1001 ACCGCCTGGA CATTAGGGCA GCCCGGATTC TTCTGGATAA TGACCATTAC
1051 GCCATGGAAA AATTGAAGAA AAGAGTACTG GAATACTTGG CTGTCAGACA
1101 GCTCAAAAAT AACCTGAAGG GCCCAATCCT ATGCTTTGTT GGCCCTCCTG
1151 GAGTTGGTAA AACAAGTGTG GGAAGATCAG TGGCCAAGAC TCTAGGTCGA
1201 GAGTTCCACA GGATTGCACT TGGAGGAGTA TGTGATCAGT CTGACATTCG
1251 AGGACACAGG CGCACCTATG TTGGCAGCAT GCCTGGTCGC ATCATCAACG
1301 GCTTGAAGAC TGTGGGAGTG AACAACCCAG TGTTCCTATT AGATGAGGTT
1351 GACAAACTGG GAAAAAGTCT ACAGGGTGAT CCAGCAGCAG CTCTGCTTGA
1401 GGTGTTGGAT CCTGAACAAA ACCATAACTT CACAGATCAT TATCTAAATG
1451 TGGCCTTTGA CCTTTCTCAA GTTCTTTTTA TAGCTACTGC CAACACCACT
1501 GCTACCATTC CAGCTGCCTT GTTGGACAGA ATGGAGATCA TTCAGGTTCC
1551 AGGTTATACA CAGGAGGAGA AGATAGAGAT TGCCCATAGG CACTTGATCC
1601 CCAAGCAGCT GGAACAACAT GGGCTGACTC CACAGCAGAT TCAGATACCC
1651 CAGGTCACCA CTCTTGACAT CATCACCAGG TATACCAGAG AGGCAGGGGT
1701 TCGTTCTCTG GATAGAAAAC TTGGGGCCAT TTGCCGAGCT GTGGCCGTGA
1751 AGGTGGCAGA AGGACAGCAT AAGGAAGCCA AGTTGGACCG TTCTGATGTG
1801 ACTGAGAGAG AAGGTTGCAG AGAACACATC TTAGAAGATG AAAAACCTGA
1851 ATCTATCAGT GACACTACTG ACTTGGCTCT ACCACCTGAA ATGCCGATTT
1901 TGATTGATTT CCATGCTCTG AAAGACATCC TTGGGCCCCC GATGTATGAA
1951 ATGGAGGTAT CTCAGCGTTT GAGTCAGCCA GGAGTAGCAA TAGGTTTGGC
2001 TTGGACTCCC TTAGGTGGAG AAATCATGTT CGTGGAGGCG AGTCGAATGG
2051 ATGGCGAGGG CCAGTTAACT CTGACCGGCC AGCTCGGGGA CGTGATGAAG
2101 GAGTCCGCCC ACCTCGCTAT CAGCTGGCTC CGCAGCAACG CAAAGAAGTA
2151 CCAGCTGACC AATGCTTTTG GAAGTTTTGA TCTTCTTGAC AACACAGACA
2201 TCCATCTGCA CTTCCCAGCT GGAGCTGTCA CAAAAGATGG ACCATCTGCT
2251 GGAGTTACCA TAGTAACCTG TCTCGCCTCA CTTTTTAGTG GCGGCTGGT
2301 ACGTTCAGAT GTAGCCATGA CTGGAGAAAT TACACTGAGA GGTCTTGTTC
2351 TTCCAGTGGG TGGAATTAAA GACAAAGTGC TGGCGGCACA CAGAGCGGGA
2401 CTGAAGCAAG TCATTATTCC TCGGAGAAAT GAAAAAGACC TTGAGGGAAT
2451 CCCAGGCAAC GTACGACAGG ATTTAAGTTT TGTCACAGCA AGCTGCCTGG
2501 ATGAGGTTCT TAATGCAGCT TTTGATGGTG GCTTTACTGT CAAGACCAGA
2551 CCTGGTCTGT TAAATAGCAA ACTGTAGGTC CAAATCTCAA TTTT (SEQ ID NO:1)
```

FIGURE 1A

FEATURES:
5'UTR: 1 - 18
Start Codon: 19
Stop Codon: 2575
3'UTR: 2578

Homologous proteins:
Top 10 BLAST Hits

	Score	E
gi|3914005|sp|P93647|LON1_MAIZE MITOCHONDRIAL LON PROTEASE HOMO...	713	0.0
gi|3914002|sp|O64948|LON1_ARATH MITOCHONDRIAL LON PROTEASE HOMO...	706	0.0
gi|3913996|sp|O04979|LON1_SPIOL MITOCHONDRIAL LON PROTEASE HOMO...	689	0.0
gi|547861|sp|P36774|LON2_MYXXA ATP-DEPENDENT PROTEASE LA 2 >gi|...	665	0.0
gi|625653|pir||A36894 ATP-dependent proteinase BsgA - Myxococcu...	661	0.0
gi|10175672|dbj|BAB06769.1| (AP001517) ATP-dependent proteinase...	581	e-165
gi|547865|sp|P36772|LON_BACBR ATP-DEPENDENT PROTEASE LA >gi|980...	573	e-162
gi|585415|sp|P37945|LON1_BACSU ATP-DEPENDENT PROTEASE LA 1 >gi|...	570	e-161
gi|547860|sp|P36773|LON1_MYXXA ATP-DEPENDENT PROTEASE LA 1 >gi|...	557	e-157
gi|7471170|pir||B75530 ATP-dependent proteinase LA - Deinococcu...	550	e-155

EST:

	Score	E
gi|9129501 /dataset=dbest /taxon=9606...	1191	0.0
gi|9150157 /dataset=dbest /taxon=9606...	1154	0.0
gi|9333228 /dataset=dbest /taxon=960...	1074	0.0
gi|10365587 /dataset=dbest /taxon=960...	1035	0.0
gi|9122839 /dataset=dbest /taxon=9606...	997	0.0
gi|9336891 /dataset=dbest /taxon=960...	969	0.0
gi|2669286 /dataset=dbest /taxon=9606 ...	890	0.0
gi|3836333 /dataset=dbest /taxon=9606 ...	767	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:
library source:
gi|9129501 Eye, retinoblastoma
gi|9150157 Skin, melanotic melanoma
gi|9333228 Uterus, endometrium adenocarcinoma
gi|10365587 Ovary adenocarcinoma
gi|2669286 Schizophrenic brain
gi|3836333 Kidney

Tissue Expression:
Human Heart

FIGURE 1B

```
   1 MSSVSPIQIP SRLPLLLITHE GVLLPGSTMR TSVDSAHNLQ LVRSRLLKGT
  51 SLQSTILGVI PNTPDPASDA QDLPPLHRIG TAALAVQVVG SNWPKPHYTL
 101 LITGLCRFQI VQVLKEKPYP IAEVEQLDRL EEFPNTCKMR EELGELSEQF
 151 YKYAVQLVEM LDMSVPAVAK LRRLLDSLPR EALPDILTSI IRTSNKEKLQ
 201 ILDAVSLEER FKMTIPLLVR QIEGLKLLQK TRKPKQDDDK RVIAIRPIRR
 251 ITHISGILED EDEDEINDDI VMLEKKIRTS SMPEQAHKVC VKEIKRLKKM
 301 PQSMPEYALT RNYLEIMVEL PWNKSTIDRL DIRAARILLD NDHYAMEKLK
 351 KRVLEYLAVR QLKNNLKGPI LCFVGPPGVG KTSVGRSVAK TLGREFHRIA
 401 LGGVCDQSDI RGHRRTYVGS MPGRIINGLK TVGVNNPVFL LDEVDKLGKS
 451 LQGDPAAALL EVLDPEQNHN FTDHYLNVAF DLSQVLFIAT ANTTATIPAA
 501 LLDRMEIIQV PGYTQEEKIE IAHRHLIPKQ LEQHGLTPQQ IQIPQVTILD
 551 IITRYTREAG VRSLDRKLGA ICRAVAVKVA EGQHKEAKLD RSDVTEREGC
 601 REHILEDEKP ESISDTTDLA LPPEMPILID FHALKDILGP PMYEMEVSQR
 651 LSQPGVAIGL AWTPLGGEIM FVEASRMDGE GQLTLTGQLG DVMKESAHLA
 701 ISWLRSNAKK YQLTNAFGSF DLLDNIDIHL HFPAGAVTKD GPSAGVTIVT
 751 CLASLFSGRL VRSDVAMTGE ITLRGLVLPV GGIKDKVLAA HRAGLKQVII
 801 PRRNEKDLEG IPGNVRQDLS FVTASCLDEV LNAAFDGGFT VKIRPGLLNS
 851 KL (SEQ ID NO:2)

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 3
      1    323-326 NKST
      2    470-473 NFTD
      3    492-495 NITA

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

          249-252 RRIT

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 11
      1     28-30 TMR
      2     35-37 SAR
      3    136-138 TCK
      4    194-196 SNK
      5    231-233 TRK
      6    327-329 TDR
      7    595-597 TER
      8    648-650 SQR
      9    757-759 SGR
     10    772-774 TLR
     11    840-842 TVK
```

FIGURE 2A

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 13

1	31-34	TSVD
2	194-197	SNKE
3	206-209	SLEE
4	257-260	TLED
5	281-284	SMPE
6	303-306	SMPE
7	281-284	SMPE
8	303-306	SMPE
9	325-328	STID
10	514-517	TQEE
11	547-550	TTLD
12	595-598	TERE
13	612-615	SISD

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

336-344 RILLDNDHY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 6

1	58-63	GVIPNT
2	378-383	GVGKTS
3	419-424	GSMPGR
4	655-660	GVAIGL
5	810-815	GIPGNV
6	846-851	GLLNSK

[7] PDOC00299 PS00342 MICROBODIES_CTER
Microbodies C-terminal targeting signal

850-852 SKL

[8] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

375-382 GPPGVGKT

[9] PDOC00803 PS01046 LON_SER
ATP-dependent serine proteases, lon family, serine active site

740-748 DGPSAGVTI

Membrane spanning structure and domains:
Candidate membrane-spanning segments:

Helix	Begin	End	Score	Certainity
1	371	391	0.652	Putative
2	488	508	1.280	Certain
3	658	678	1.117	Certain
4	747	767	1.430	Certain

BLAST Alignment to Top Hit:
>gi|3914005|sp|P93647|LON1_MAIZE MITOCHONDRIAL LON PROTEASE HOMOLOG
1 PRECURSOR >gi|7428224|pir||T04321 endopeptidase La homolog (EC 3.4.21.-) LON1 precursor, mitochondrial - maize >gi|1816586|gb|AAC50011.1| (U85494) LON1 protease [Zea mays]

FIGURE 2B

```
          Length = 885

 Score =  713 bits (1821), Expect = 0.0
 Identities = 401/897 (44%), Positives = 562/897 (61%), Gaps = 65/897 (7%)

Query: 3   SVSPIQIPSRLPLLLTHEGVLLPGSTMRTSVDSARNLQLVRSRLLKGTSLQSTILGVIPN 62
           S SP+++PSRL +L     VLLPG+ +R    +  +++LV   L +    + ++GV+P
Sbjct: 2   SDSPVELPSRLAVLPFRNKVLLPGAIVRIRCINPSSVKLVEQELWQKE--EKGLIGVLPV 59

Query: 63  ------------TPDPASDA----------------QDLP----PLH--RIGTAALAVQV 88
                      +P   SD+                  QD      P+H    G AA A+ +
Sbjct: 60  RDSEATAVGSLLSPGVGSDSGEGGSKVGGSAVESSKQDTKNGKEPIHWHSKGVAARALHL 119

Query: 89  V-GSNWPKPH--YTLLITGLCRFQIVQVLKEKPYPIAEVEQLDRLEEFPNTCKMREELGE 145
             G   P     Y +++ GLCRF + ++    PY +A V +LD  +      +   +L
Sbjct: 120 SRGVEKPSGRVTYIVVLEGLCRFSVQELSARGPYHVARVSRLDMTKTELEQAEQDPDLIA 179

Query: 146 LSEQFYKYAVQLVEMLDMSVPAVAKLRRLLDSLPREALPDILTSIIRTSNKEKLQILDAV 205
           LS QF   A++L+ +L+     V + + LLD++P   L DI  +    S +E+L +LD+V
Sbjct: 180 LSRQFKATAMELISVLEQKQKTVGRTKVLLDTVPVYRLADIFVASFEISFEEQLSMLDSV 239

Query: 206 SLEERFKMTIPLLVRQIEGL----KLLQKTRKPKQDDDKRVIAIRPIRRITHISGTLEDE 261
            L+ R      L+ R ++ +    K+ QK          K  +  +R I    G
Sbjct: 240 HLKVRLSKATELVDRHLQSILVAEKITQKVEGQLSKSQKEFLLRQQMRAIKEELG----- 294

Query: 262 DEDEDNDDIVMLEKKIRTSSMPEQAHKVCVKEIKRLKKMPQSMPEYALTRNYLELMVELP 321
           D D+D DD+  LE+K++ + MP    K   +E++RL+KM    P Y+ +R YLEL+ +LP
Sbjct: 295 DNDDDEDDVAALERKMQNAGMPANIWKHAQREMRRLRKMQPQQPGYSSSRAYLELLADLP 354

Query: 322 WNKSTTDR-LDIRAARILLDNDHYAMEKLKKRVLEYLAVRQLKNNLKGPILCFVGPPGVG 380
           W K + +R LD+R A+  LD DHY + K+K+R++EYLAVR+LK + +GP+LCFVGPPGVG
Sbjct: 355 WQKVSEERELDLRVAKESLDQDHYGLTKVKQRIIEYLAVRKLKPDARGPVLCFVGPPGVG 414

Query: 381 KTSVGRSVAKTLGREFHRIALGGVCDQSDIRGHRRTYVGSMPGRIINGLKTVGVNNPVFL 440
           KTS+  S+AK L R+F RI+LGGV D++DIRGHRRTY+GSMPGR+I+GLK V V+NPV L
Sbjct: 415 KTSLASSIAKALNRKFIRISLGGVKDEADIRGHRRTYIGSMPGRLIDGLKRVSVSNPVML 474

Query: 441 LDEVDKLGKSLQGDPAAALLEVLDPEQNHNFTDHYLNVAFDLSQVLFIATANTTATIPAA 500
           LDE+DK G  ++GDPA+ALLEVLDPEQN  F DHYLNV FDLS+V+F+ ATAN    IP
Sbjct: 475 LDEIDKTGSDVRGDPASALLEVLDPEQNKAFNDHYLNVPFDLSKVIFVATANRMQPIPPP 534

Query: 501 LLDRMEIIQVPGYTQEEKIEIAHRHLIPKQLEQHGLTPQQIQIPQVTTLDIITRYTREAG 560
           LLDRMEII++PGYT EEK++IA +HLIP+ LEQHGL+   +QIP+     +I RYTREAG
Sbjct: 535 LLDRMEIIELPGYTPEEKLKIAMKHLIPRVLEQHGLSTINLQIPEAMVKLVIERYTREAG 594

Query: 561 VRSLDRKLGAICRAVAVKVAEGQHKEAKLDRS---------DVTEREGCREHILEDEKPE 611
           VR+L+R L A+ RA AVKVAE Q K  +L +           D    +G    +
Sbjct: 595 VRNLERNLAALARAAAVKVAE-QVKTLRLGKEIQPITTTLLDSRLADGGEVEMEVIPMEH 653

Query: 612 SISDTTDLALPPEMPILIDFHALKDILGPPMY-EMEVSQRLSQPGVAIGLAWTPLGGEIM 670
            IS+T +       P+++D   L+ +LGPP + + E + R++ PGV++GL WT +GGE+
Sbjct: 654 DISNTYE----NPSPMIVDEAMLEKVLGPPRFDDREAADRVASPGVSVGLVWTSVGGEVQ 709

Query: 671 FVEASRMDGEGQLTLTGQLGDVMKESAHLAISWLRSNAKKYQLTNAFGSFDLLDNTDIHL 730
           FVEA+ M G+G L LTGQLGDV+KESA LA++W+R+ A    L+       +LL++ DIH+
Sbjct: 710 FVEATAMVGKGDLHLTGQLGDVIKESAQLALTWVRARAADLNLSPT-SDINLLESRDIHI 768

Query: 731 HFPAGAVTKDGPSAGVTIVTCLASLFSGRLVRSDVAMTGEITLRGLVLPVGGIKDKVLAA 790
           HFPAGAV KDGPSAGVT+VT L SLFS R VR+D AMTGE+TLRGLVLPVGG+KDKVLAA
Sbjct: 769 HFPAGAVPKDGPSAGVTLVTALVSLFSNRKVRADTAMTGEMTLRGLVLPVGGVKDKVLAA 828

Query: 791 HRAGLKQVIIPRRNEKDLEGIPGNVRQDLSFVTASCLDEVLNAAFDGGFIVKIRPGL 847
           HR G+K+VI+P RN KDL  +P  +  D+  +    ++EVL+ AF+G   +++R  L
Sbjct: 829 HRYGIKRVILPERNLKDLSEVPLPILSDMEILLVKRIEEVLDHAFEGRCPLRSRSKL 885 (SEQ ID NO:4)
```

FIGURE 2C

Hmmer search results (Pfam):
Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00004	ATPases associated with various cellular act	121.1	4.3e-33	1
PF01202	Shikimate kinase	27.1	1.4e-06	1
PF00005	ABC transporter	7.6	0.49	1
PF01695	IstB-like ATP binding protein	6.5	1.4	1
PF00495	Chaperonin clpA/B	5.9	0.92	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF01695	1/1	371	382	..	52	63	..	6.5	1.4
PF00005	1/1	368	383	..	1	16	[.	7.6	0.49
PF00495	1/1	373	393	..	74	94	..	5.9	0.92
PF01202	1/1	369	396	..	1	28	[.	27.1	1.4e-06
PF00004	1/1	370	565	..	1	220	[]	121.1	4.3e-33

FIGURE 2D

```
   1 ATCATTAAAA AGTCAGGAAA CAACAGGTGC TGGAGAGGAT GTGGAGAAAT
  51 AGGAACACTT TTACACTGTT GGTGGGACTG TAAACTAGTT CAACCATTGT
 101 GGAAGACAGT GTGGCAATTC CTCAAGGATC TGGAACTAGA AATACCATTT
 151 GACCCAGCCA TCCCATTGCT GGGTATATAC CCAAAGGATT ATAAATCATG
 201 CTGCTATAAA GACACACACA CACGTATGCT TACTGCGGCA CTATTCGCAA
 251 TAGCAAAGAC TTGGAACCAA CCCAAATGTC CATCAATGAT AGACTGGATT
 301 AAGAAAATGT GGCACATATA CACCATGGAA TACTATGCAG CCATAAAAAA
 351 GGATGAGTTC ATGTCCTTTG TAGGGACATG GATGATGCTG GAAACCATCA
 401 TTCTGAGCAA ACTATCGCAA AGACCGAAAA CAAAACACTG CAAGTTCTCA
 451 CTCATAGGTG GCAACTGAAC AATGAGAACA CTTGGACACA GGGTGGGGAA
 501 CATCACACTC AGGGGCCTGT CGTTGGGTGG TGGGGAGTGG GGGGGAAGGG
 551 ATACCATTAG GAGATATACC TAATGTAAAT GACGAGTTAG TGAGTGCAGC
 601 AAACCAACAT GGCACATGTA TACATATGTA ACAAACCTGT ACGTTGTGCA
 651 CATGTACCCT AGAACTTAAA CTATAATAAA AAATAAAATT AAATTAAAAA
 701 CATGAAAAAA AATAAAAGTA TCAAGGTTGT AAAAAAAAAA AAAATTGGAC
 751 GGGCGCAGTG GCTCAGGCCT GTAATCCCAG CACTTTTGGG AGGCCAAGGC
 801 GGGCAGATCA CTGAGGTCAG GAGATTGAGA CCATCCTGGC TAACATGGCG
 851 AAACCCCGTC TCTACTAAAA ATACAAAAAA TTAGCCGGGC AGTGGTTGCG
 901 GGTGCCTGTA GTCCCCAGCT ACTCGGGAGG CTGAAGCAGG AGAATGGCAT
 951 GAACCCGGGA GGCGGAGCTT GCAGTGAGCC GAGATCTCGC CACTACACTC
1001 CAGCCTGGGT GACAGAGCGA GACTCCGTCT CAAAAAAAAA AAAAAAAAAA
1051 AAAAATTGAG GACTTGCCAC AGATTAGAGA ACACCTAGGA GATTTCATAA
1101 CAAAACACCT AGGAGATTTC ACAACAGGAT CCTGGATATT GGATCCTGGA
1151 CCAGATCCAA TGAAGGACAT TAGTGGGAAA ACTGGCAAAA TTTGGGTAAG
1201 GCCTATAGGT TAAACGATAA TAATGTTAAT TTCCTGGTTT TGATCATTGA
1251 ACTATGATTA TGTAAGATGA TAACAGACGA AACTGGGTGA AAGGTATATA
1301 GGAACTCTGC TGTAGTTTTG TACATCTAAA ATCAATTCGG GCCGGGCACG
1351 TTGGCTCACG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GTGGACGGAT
1401 CGCTTGAGGT CAGGAGTTAA AGACCAGCCT GGCCAACATG GTGAAATCCC
1451 CTCCCTACTA AAAATACAAC AATTAGCTGG GTGTGGTGGC GGGCATCTGT
1501 AATCCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATCGCTT GAACCCGGGA
1551 GGCAGAGGCT GCAAGCCGTG GGTATCGCGC CATTGCACTC CAGCCTCCGC
1601 GACAGAGCGA GAATCTGTCT CAGAATAAAT AAATAAATAA ATAAATAAAT
1651 AATTAGTTCG AATCAAAAGT TAAAAACACT TCAAGTATAT GTAAAAAATC
1701 GAAGAAAACG TTAAAAACAC TTCAAGTATA TACAATTCAA ATAAGATCAT
1751 CCTTCCAAAT ATACTCTGTA AGTGAGGCGA AGGTCGCTGC ACGCTTGAGT
1801 GCACGTCTTT CCGCATAGGT AGGACGCTCA AGTCTTACCG GGAGGCTCTC
1851 CTAGAGAGCA GCGCGAAGCC ATGGCTTTTG GGCCCGGGGA CGGACCGTAG
1901 CGCGTAGCCG GAAGCGGAGG CGTGGAGGCG GGTCTGAGGT TTGGTGACTG
1951 CGGGGCAGGC CGGGGGCAGC TGTCTGTCTG GCTCTTTTTG ACAGCCCCCA
2001 GTGCGAAAGG CTGCCAGCAT GTCATCAGTG AGCCCCATCC AGATCCCCAG
2051 TCGCCTCCCG CTGCTGCTCA CCCACGAGGG CGTCCTGCTG CCCGGCTCCA
2101 CCATGCGCAC CAGCGTGGAC TCGGCCCGCA ACCTGCAGCT GGTGCGGAGC
2151 CGCCTTCTGA AGGGCACGTC GCTGCAAAGC ACCATCCTGG GCGTCATCCC
2201 CAACACGCCT GACCCCGCCA GCGACGCGCA GGACCTGCCG CCGCTGCACA
2251 GGTAGGCCTG GCTGCCCCCG CGGCGGCGGC GGGCGGCGCG GCCTCCTCCG
2301 GGGACCTGGG CCCAGGCCAC GGCCTGCCTT GAGCGCGAGG CTCAGTTCGG
2351 GGCGGCCTTC GCGGCTCGGT TCCGCCTCTC TGGTGCTATC ACTTGCAAAA
2401 TGGGGATGTC AGATACCTGC CCCATGACCA TGAATGAGAT CGTTCATGAA
2451 GTAGTGCCTG ACACCTGGTG AAACTACGCA GTTCCCTACC GTTCTGGATA
2501 ATTTAATTTG AATCCTCTTC CCCCTCTCCG CAATTCCTCG CCCTCGGTCT
2551 TCAGCCTCCT AGGCCAGTGC TTTTAACTTT CCAGGCCCTT TCTTTCTCCC
2601 CGGTGATCTC TGCCTTCACT TGCCTTCGCT TTTCACCTTT CTCCCCACTG
2651 CCCTTTACTC CTATCCGCCT CCCCTTTTCT GTCACCCATC ATTTTTGTCC
2701 GCTGAGGCAT TCTCTGCTCC GTGAGTTTTA ACTTTTCCTG TTTCATTCCT
2751 AAACTGCACT ATTTGTGGGT GCCTTTCTTC TATACTCCCT GCCACCCTTC
2801 TCCTTCTCCC CCTAATCCTT CTGTTTCCCT TTGTAAAGGG CCTTTACTGC
2851 TCACATTTTC GCTGGTCCCC CTTTCTGGAA CTTTCCTAGC TTCTCACCTC
2901 TGCTCCTTCA CTCATAACAT TTCTTAGGCC CCAGGCTTAC TACTATATTG
2951 CCCAGTACCC TCGCCCTATT GGTGTGACTT TGGGTGAGAG CTTTAACCTC
3001 TATTTCTTTT ATTCTGCAAT TTGGAAACTG ACAGCATCCA TCTCTTAGGC
3051 AAGTTATGAA GAATAAATTG AATAATGTGT ATATTCCACT TTGCACCATG
3101 CATGATGGAT GACTTTGCTG TCCAGTACTG TGTAGTGCAT GTGGCTCGTC
3151 AAATTGAGAT GATAGAATTG CCAGTTGTCC TGGTTTGCTG CGATTGTCTG
```

FIGURE 3A-1

3201 TTTTAGCATT GAAAGTCCTA TGTTTTAGCC CCTCCGTCCC AGGGAAACCA
3251 GGAGGTTGGT CACCCTAAAT GTGCTGTAAG TGTACAATAC ACGCCAGATT
3301 TTGAAAAAAC TTTTTGATTA ATACATTTTA TATGGATTAA ATGTTGGAAA
3351 GGTAATATTT TGAGTACTTG GGGTTAATAA AATGTTAAGA TTTCTGCTGT
3401 TTTTACTTTA TAATGTGGCC ACTAAAATTT TATATGTGGT CCACATTATA
3451 TTTTTATTGG ACAATGCTGG TATATCGTAT GCTCTCAACA AGTATCTTCA
3501 AACTCACCTG CCAAGCACCC GCCTCCTATT CCTAACTCTA CTGGAGGTGT
3551 TGTGTTTTCA GTTTAGAGCT TCTCCTTTCC TGGCAGTTAT CCCTTATTTT
3601 TAAATTAGGG GTTCCTGACT CTGAATGGAT TTCCGGAGGG TTGGACATGT
3651 CTTATTTTTC CTCAAAATCT TGTGACTATG TACATTTTTT TAGGAGAATC
3701 CTTTGCTTTC TTCAGATTCT CAAAGGAGAC TGGTACCTCC CCCCACCCCC
3751 GTTAAAAGAA AGCAAAACAA AGCAACAAAG ACCAACAAAC CTTCCACAGC
3801 AGCCCAGTAT TCATTTATAT TGTAAAAGCC TTGATTTTCT CAAGCATGGA
3851 AAATATTTTG GCTCCCATCT GACCTGCTTT GGTTATTGCC TGAGTGGAAT
3901 TGGTCACATT CCAAGTTTCA GTACTCTTTG ATAAATTGTA TTGGATTCTA
3951 GTTTCCCAAC ATACGACTCT GCTCCTTCTG CTTACTTTTC CCAAATTATT
4001 TTGCCTTCTG TGCCCAGGCA CACTTAGTTC CCTGTCTAGG CAAGAGTGGT
4051 CATTATTAGA CTTCATTTTC TTTCTACTGT GCATATGTAT TGATTAGCCA
4101 TGGGCACATT GTGAACTTGA AAAGTCGATT TAGTCACATT TTAAGTTTCA
4151 CTATTTGTTG GTATTATTCT GGCAAGATTT TGGAAGGTTT TTATTATTTA
4201 TTCATTTGTG TATTTTTTGA GACAGAGTCT CATTCTGTCT CCTCCGCTGA
4251 AGTGCAGTGG CGTGATCGTA GCCCACCGCA ACCTTGATTG AACTCCTGGG
4301 CTCAAGTGAT CGTCCTGCCT CAGCTTCTGG AGTGGCTGGG ACTATAGGCG
4351 TGCACCACTA CACCCAGCTA ATTTTTAAAT TTTTGTAGA AATGGGGTCT
4401 CACTATGTTG CTTAGGCTGG TCTCAAACTC CTGGACTCAA GCTATCCCCT
4451 GCTTTGGCCT CTGGAGTAGC TGGGACTATA GGCAAGCGCC ACCATACCCT
4501 TCAGGTTTTT AATTTATTTT ATGAAAATCC CTCCAAAGCA ACAATCCTCA
4551 ATTCTCCTGC TTGAAAGTAA TCACTAATAA TCAGGTACTG TGTGATCTGA
4601 TCCTTGATGT TCATATTATT GCCTTTAACT GAGTAGCAAT GTTAAAATTT
4651 AATCATTTAA ATTAGAAAAC ATATATTGAA AAGTCTTCAT AGAAGTCCGG
4701 CATTATAAGA ACTCATCAGA CCATCTAGTT ATCCTAGAAG TATTGTTTGC
4751 TACTTAAAAA GCCTATGTGG AAAGATTGTA CCATATTCCT TGGTAATAGT
4801 TTCCAATGTC TTTTTTTCTC TAATAGGGCC TTTAAAACAC TCTACTTAAA
4851 AAAAAAAAAA AAAAAAGCT TTAACAATAC CAATACTGAG TAATCCATAG
4901 CATTAGCCTG TTTCCACGCA CAAGTCTGTC CTTCCCCAGT TACCTGCTTT
4951 TCTGTATGGT AGCCCAGAGG CCAGAAGAGG GGCTCTGTTC CTTTCTCTTG
5001 TTTCCTTTGC GCTATCCAGG TGACGCTGGC ACAGCCTTCA AAGAGCAGCA
5051 GAAGTAATTT GCTCCCAGCG TTCTTTGCCA CATAGAGTGG CAGGGTTAAA
5101 TGATTTAAAA TTTAATCATT TAAATTAGAA AACATAGATT GAAAAGTCTT
5151 CATAGAATTC CAGCATTAAA AGAACTCATC AGACCATCTA GTTATCCTAG
5201 AAGTATTGTT TGCTACTTCA AAAGCCTATG TGGAAAGATT GTACGATATT
5251 CCTTGGTAAT AGTTTCGAAT GTCTTTTTTT CTCTAATATG GCTTTTAAAG
5301 CACTCTACTT AAAAAAAAAA AAAGCTTTAA TAATACCAAT ACCGAGTTAT
5351 CCACAGTATT AGTCTGTTTC CATGCACAAA TCTGTCCTTC CCCAGTTACC
5401 TGCTTTTCTG TATGGTAGCC CAGAGGTGAG ATGAGGGCCT CTGTTCCTGT
5451 CTCTTGTTTC CTTTACACCA TCCAGGTGAC ACTGGCTGCA GCCTTCAAGG
5501 AGCAGCAGAA GTAATTTGCT CCCAGCGTTC TTTGCCACAC AGAGTGGCAG
5551 GATTAGATGT TGACTTACCT CTGCCACTTC CTTGGTGGTT TTGAGTAGTA
5601 CAGTCCCTTT CTGCACGTTA GTGTGCAGGC ATGTTGCCTG CAGGAGCCTT
5651 TTTAAAGGAG GAGCTTTGGA CTTGTCCTGC AGTATAGAAC TTGGCTGGCA
5701 TGCTGACCCA GGGCACCCTG CATTTTTCTG CTTAGTAGAA CTGCATTTTT
5751 AGTGCTTCCT GAGTGACCCA TTGTTTTCTT AGTGAAAAGG GGTCATAATT
5801 TAGTACTACC TGTACAATAT CCTTTCAAGC ATTTCAAGAT GGTCATCCAG
5851 CTTTCTTCCA AATTTACACT TTTCAGGGTA CATGGCTTCA TTTCCTCATA
5901 GTGCCGACTT CTCAGTCTCC CTCACCAGGC TGGTGTCAAA CTTGTGAGCT
5951 CAAGTGATCC TCCTGCCTCT GTCTCCCAAA GTGTTAGGAT TACAGGCGTG
6001 AGCCACCATG CCTGGCCTAT GTTTATAATT CTTGTAGGTA GAAGTGGTAC
6051 CTATTGTCCA TTGTAATGAG AAAAAAGTAA AATTTGTCTT AAAATATAAT
6101 TAAGGAACTC AATTTATTAA ATTTAAATTT ATCCTTTAAA TTTTAAATTT
6151 AAATTTATTT CTTAAATTTA TTTCTATTAC ATTTTCTTGT AACCATGTAC
6201 ACCTAAGTTG TTCTACTTTA ATTTTTTTGA GACAGGGTCT CACTCTGTCA
6251 CCCATGCTGG TGCAGTGGTG CCATCTCAGC TCACTGCAAC CTTTGCCTCC
6301 CAGGTTCAAG TGATCCTCTC ACCTCAGCCT CCTGAGTGTC TGGGATTACA
6351 GGCATGTGCC ACAATGCCTA GCTATTTTTT TTTTTTTTTT TTGGTGGAGA

FIGURE 3A-2

6401 CGGGGTTTTG CCATGTTGCG CAAACTGGTT TCGAACTCCT GAGCCCAAGT
6451 GATCCACTTG CCTCGGCCTC CCAAAGTGCT GGGATTATAG GTGTGAGCCA
6501 CCATGCCATG TTCTACCTTT TTGAATCTCA TTTACTCACT TGTAATAAGG
6551 AAATAATACT ACCTTCTTCA TGGGGTGAAG GGAGGTATAA AATGAAGTAT
6601 ACATATGAAA GCCTTTTGAA ACTGCAAAGC ATTCTAAACC TATATCCAAA
6651 TGGGTAGTTT TAAATGTAGA TTTTCACAAA AGGGGATTAA AGAGAGGAGT
6701 GGGGAGGCCC CATATTATTC CAACACGGGC TGAACTGAAC TAACATCATT
6751 GCAGGAAGGT CTTGGAAGAT TAAAGATTCC AAGAAAAATT AAGGGCTTTG
6801 AGTAAAAAAA TTTTTTAAAA GTGGCTGGGC CTGGTGGCAC GTGCCTGTAC
6851 TCCCATCTAC TCATGATGCT GAGGCGGAGG ATTACTTGAG CCCAGGTGAT
6901 CGAAGCTGCA GTGAGCTATA ATCGTACCAC TGCACTCCAG CCTGGGTGAC
6951 AGAGCAAGAT TCTGTCTATA GGAAAAAAAA AAAAAAAAAA AGCAAGTGCT
7001 GGGCATATAG GCTGGAATTA GATATTTACA TAATATCCTC ATCTTGGAAA
7051 ACTTTTTCCA GTAGTGCTGC TTTTAGATTT TCCCACTACT GCAGTTGATG
7101 GTTCTTAAAT ATGTTTGGAA CTCTTATATT ATTTAGGTCA GTTTCCAAAT
7151 TACACAAATT GTAACCATTG TAGTCAGACC TCACTTGAAT GAAAACAATA
7201 TTTTACAAAC TCTGAGGGTA GATTCGAGTT AGGATTTGGA TTAAAACATT
7251 ATCTTAAAAC CTCTGAGGGT AGATTCGAGT TAGGAGTTTC AAAACTTCTT
7301 TGAACAATAT CATAATTAGG ATGTAGATTT ACAGAGCTAC TAGCTAAAGG
7351 GAAGGACACC AGTCATTGGG ATGTATAAGT TTGGATCTGT TGCAAAATTA
7401 AAATGCTGCC TTTTGAGCAT GCCTAATAAT GCACATACAA TAGAAGAGCC
7451 AGAATTTTTA GAAAAATGAC TGACTTGATA TACAACCTTT TGTATATCAT
7501 AGAAGGAAAA TATTAGTTGA GTATTTTGTT TATTTACCTG TTTGTATATA
7551 TAAAACCTGG GGCCCAATAT ACAATAGATT CTTTTTCACT ATGCTTTTCA
7601 CCCACAGTGT CTCACCAGGT ACTCTGTTTC TAGCCATCTA TAATTTCATA
7651 GATGTTTTTC TTTAAAAGGG ATGTATTCTA GGCTGGGCGA GGTGGGTCTT
7701 GCCTGTAATC CTAGCACTTT GGGAGGCCAA GATGGGAGGA TTGCTTGAGG
7751 CCAGTAGTTG GAGATCAGCC TGGTCAACAT CATGAGATCC CATCTCTGTT
7801 AAAAAAAGAA AAAAAAATTT TTTTAAAGGG ATAATTTCTA GTCAACTATA
7851 AGTGATTTTA AGTAAAAAGC AATTAAGGCA TGTATACATC TGTACCTTTT
7901 GTAGGCATAG TATAAATTCA GCTTAATCTC TTCAGTTTGG AACATCTTCC
7951 TTTCACAGCA AAAATATTGT ATTTGCTTTA TAAGAAAACC CCTTTTGGCC
8001 AGGTGTGGTG GCTCACGCCC GTAATCCTAG CACTTTGGGA GGCTGAGGTG
8051 GGTGGATTAC CTTAGGTCAG GAGTTCGAGA CCAGCCTGGC CAACATAGTG
8101 AAACCCTGTC TCTACTAAAA ATACAAAAAT TAGCTGGGCG TGGTGGTGTG
8151 TGCCCTGTAA TCCCAGCTAG TTGGGAGGCT GAGGCACGAG AATCCCTTGA
8201 ACCCAGGAGG CAGAGTGCAA TAAGCCGAGA TCACGCCATT GTACGTCAGG
8251 CTGGGCGACA GGGTGAGACT CCCTCTAAAA AACAAACAAA AAAACCACAG
8301 TGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCCAAGG TGGGCGAATC
8351 ATGAGGTCAA GAGATCGAGA TCATCCTGGC CAACATGGTG AAACCTCATC
8401 TCTACAAAAA ATACAAAAAA TTAGCTGGGC GTGGTGGTGT GTGCCTGTAG
8451 TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG AATCACTTGA ATCTGGGAGA
8501 CGGAGGTTGC AGTGAGCCAA GATTAGGCTA CTGCGCTCCA GCCTGGTGAC
8551 AAAGTGAGAC TCCGTCTCAA AAAAAAAAAA CAAAAAACAA AAAACAACTC
8601 TTTAGCATCA CCTTTTAGCA ATGACATAGC CCAAATAATT AAATTTGTCT
8651 CCTGATCGGA GATTTGGATT TGTCTCATCT CTCTTTCTGG TTCCTCCTTG
8701 GTTTCTACTT TGTAAACCCT TTAGGCCGGG GATCCAGTTT CTTGTCTGTG
8751 GATGTTTTAT ATACAAACAG GACTGTGAGC TCTTTCAGCA TTGTACAAAC
8801 AGTGATGAAT ATCATCTGCA ATTAATTATG TTTAAGTTAT TCTCTAATCA
8851 GTTTAGAGGT GGCTCACTTC CTCAGGCAAT CTGAGTGGGC TTTCAGGAAG
8901 TGGGAAATAT TATCTACTAT TGATTGAAGA AAAGCAGCCA CAACACAAAT
8951 AAGTCAAAAT AATAGCTAAT TGCTAAATAA TTTCAAGTTT TTTATGTATG
9001 TGATTTTTTT CCCTCACCAA TTTATCTTCT CAGTTGTTTG GCTTATTATT
9051 TAAATCAGTT TTTATTGTAA ACATGGTAAT GACTGAAAGG TAAGAAAAGG
9101 ATAGACGTAG TTCAGAATAA ACTGAGTGGC AGAAAGAAGC CAAAGGCTAT
9151 GTGTAATCTA CGGAATGAGT AATTTATAAG GAAGTAATCA AGAATTCACT
9201 GTGTATAGAA GTAAGCAAGT TCACTCACAT AGTCACATAC TGTATTACAT
9251 GATTTATTAT CTTTGAGATG GGCAGGTGTG GTGTTCTTCT ATTACCGCTT
9301 TCCTAGGGTG TTGAGAGTTC TAGTCCTTCT ATTTTCTTTT CTGGAATTAC
9351 CACTTTTCCT ATGGCTGAAG GGAGAAAATA TTATTTATTT TGGGATCTGG
9401 AATTGTCTTC TCAATGTTGA TTTTTGTATT TTATATAACT GACTTAGTTT
9451 GGATGAGGCT TCCTTTCTGT GAATTAAATT TATATGTGAC TTGATCAGAG
9501 TTGTATTTGC TGATGAGGAG CTGAGACTTG AAGCCTTTTC ACCTATTGTT
9551 AGGTAAAATG ATTACCACTT AGAACTAGGT TGAGACCTTT TGAGATGTGG

FIGURE 3A-3

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 9601 GTCTTTCTTT AGCTCTCCTC AGTCTATGGC AGTGTGTGGA CTGTAATATT
 9651 TAGCCCTCAC ACTTAGAAAT TCAGTGTTAA GGGCATATAT ATAAGTTCCC
 9701 AGTATGTGAT GGCAGCTTGT GATAAGGTGG GTATGTGGAA GTTTCATAGA
 9751 CTGATTATGT AAGAAAACTG ACTTGATGTT AGTAGCACAA CTGGTGTTGG
 9801 AACGGAGATT TCTTAGATTG GTTTATGCTA TTTATATTTA AATGTATTTA
 9851 AATTGATAAT ATTTATCCTG GTATAAGATT GCCTTATTCT TAGTTGACAA
 9901 TGTTAATTTA AGATATGTAA TTCTCAGCTG CTTTTCTCTT ACATTTTTAC
 9951 GCTTGAATAA TCCAAGTGTT TACAAATTCC TACCTAATTT TTTAAAAGAG
10001 GTGCAGATTA TAGTGAGATG GTCTGCTTTG CCATATAGCT GAGGGTAGTG
10051 GCAGAAGAGG CCACATACTG GATGCTAAGT TAAATAGAGA AAAAATTTAT
10101 TTACACTTCA GATGTCTTTT GCTTAATGAA TGTATCAGAA AAGCCAACAC
10151 TTTCTGAAGT GAGTTTCTGT TCTACCGTAT TGAATGTTTG TAATACCGAT
10201 GTTTTGTGTG TTTTTCAGGA TTGGCACAGC TGCACTGGCC GTTCAGGTTG
10251 TGGGCAGTAA CTGGCCCAAG CCCCACTACA CTCTGTTGAT TACAGGCCTA
10301 TGCCGTTTCC AGATTGTACA GGTCTTAAAA GAGAAGCCAT ATCCCATTGC
10351 TGAAGTGGAG CAGTTGGACC GACTTGAGGA GTTTCCCAAC ACCTGTAAAA
10401 TGAGGGAGGA GCTAGGAGAA CTATCAGAGC AGTTTTACAA ATATGCAGTA
10451 CAAGTAAGTT GCTTTTATTT TTTCTTAAAA CCCATTTTTC TTTGGTTCTT
10501 TTGCTTTCCT AAGATATGGT GAATCTGTTG GATAGTGAAG TTTTAGGACA
10551 GTATACATTT AAATGAGTTA GTAACATTAT ATATTAATTC TGATTTACTC
10601 TTATCTGGGG TTGTACCTAA ATCATTCCAG GACATATTGG CCTACCCTTT
10651 CTAAAGTTTT CCAAATGTTA TTTCTACAGC TTTCCTTCTA ACTTCTACTG
10701 TCTCTAAACT AGATAATTAT TAAACCTAAA TATTTAAAGC TAAAAAACGA
10751 AATACTGCAC AGAAGCTGTC TGTCACTAAA ATATCTAGGC ACCATTTATA
10801 TAAATTACAA TATATTACTT CAAAAGTCAA GATCACATTG TCTAGCAGTA
10851 ACTATGGTAG ATCAAGCCTG TGGTGGGCTG ATTTCAAGTA TGGTTAAAAC
10901 CTTGATTAAC TAGAATGCTG GGAAGGAAGC ACATTTTAGA TATGCATTAA
10951 ATATTTGACT CTTTAATTCT AGTTCTTTTT GGTTAACTCT AGATAGAACA
11001 GAAAGCTCCT ATTCCCACCC CATTTTGTTT CAAACCTTAA TGAAACATAA
11051 AATTATAAAG TATAGTCTTC TACTTTTCTA TTAGTTTAAT CCAGTGACTA
11101 TAACTAGATC TATGAGGATC AGATAATGTT TAAAAGTCAC AATTATAAAT
11151 ACTACTGATC ATTGAAATAT GTGTGGGGCA AGTGTTCATA GCCAGTGGTA
11201 TTTGTATCTG ATGTGGCATT TGAAGAGCCA TACTTACAGT GTAATGAACA
11251 ATAACAGAAA AATAGTAAAT TTGAGGGCCA GGTGCGCTGG TGCACACCTG
11301 TAATCCCAGC ACTTTGGGAG GCTGAGGTGG GTGGATTGCT TGAGCCCAGT
11351 AGTTCGAGAT CAGCCTAGGC AGCATGGTGA GATCCCGTCT CTACAAAATG
11401 TACAAAAATT AGCCGAGTGT GATGGTGCGT GCCTGTAGTC CCAGCTACTG
11451 GGGAGGCTGA GGTGGGAGGA TTACTTGAAC CTAGTAGGTG GAAGTTGCAG
11501 TGAGCCAAGA TTGCATCACT GCATTCCAGC CTGGGCAACA GAGCGAGACC
11551 CTGACTCAAA AAAAAAAAAA GAAAAATAGA AAATTTGAAT CTGTAATTTC
11601 TATATGGGCT GAAAGAAAGC ACTTTGAGGA AAGAAATTTC AGTTTGAAAA
11651 CTGGAATAAG TGAATATACT GCTTAGGAAT AAAGGAGATT GAGAGAAATA
11701 GAATTTCTTT TTCTTTTCAG CAGTGATGTT CCCTGGGTCT TTGTGCCTCT
11751 ATTGGACATA GATAGCTTCA TAGCCTCTTT TGCTTTGCTT TTACTTCTTT
11801 GTACTTTGAA TCTAGAGGAA CTTTTTAAAC TTGTAAAGAT TTTGCAGTGA
11851 CATTAAAGGA ATTTTTAGAA ATAAATAGAT CACCACACAT CTTACTGTCA
11901 TCATGCATCA AATTTAATTT TTGTTCGTCT TCTGGGCTCA GTTCATATTC
11951 AATTATATGT TTTGTTTTTG TATCCATGTC TGATGTTCAT ATTAAGTACT
12001 TTTGTTAATT TCATTGAGTT AATGTATACT AATTTTATAA TTTCTCTTTT
12051 TAGACATTAA AGTTATTTCC AATTATTCTC TTTCATCCCC TTCTGCATCT
12101 ACTTCTACTT CTGCATCTCT TCAATGAACT TCTTCAATAG CATCCTGTCT
12151 CCTAGTTCTT CTGTCTTGAA CCTTTTCTCT TCACTGAGCC TTTCTAAAAG
12201 AAGTCTGGGG CATCCCATTC CCTTGAGTAA AAGACTTTAA TGGCTATAGG
12251 ATGGACACCA AATTTCTTAG TATAACATTA AGACCGTTTG CAACTTGTCT
12301 TGGGCCTATC TGTCTTGCGT CAACTCTAGT TATCACCTCA CTGACACCCT
12351 AGTTCTAGCT CTACTGAATG TAAAACAGCT TCACATTGAG TTATTTTATG
12401 TCTCTATGAT TCTGCCTTCA GTTCTCTGCT GGGAGTGCTC TTCCATCTCT
12451 GATTTTTTTT TTTTTTTTTG AAATGGAGTC TTGCCCTGTT GCCCAGGCTG
12501 GAGTGCAGTG GTGCAATTTC GGCTCACTGC AGCCTCCGCC TCCCGGGTTC
12551 AAGCGATTCT CCTGCTTCAG CCTCCCAAGT AGCTGGCATT ACAGGCATGC
12601 GCCACCACGC CCGGCTAACT TTTTGTGTCT TTAGTAGAGA TGAGGTTTCA
12651 CCATGTTGGC CAGGCTGGTC TCGAACTCCT GACCTCATGA TCCAACCGCC
12701 ACCACGCCCG GCCTCCATCT CTGAATTTTA AAATTGAATC TATGCTTTCC
12751 CAACAGCTGT AGGCTGTTAG CGCTCATCTC TGTGTGCCTT CACAGTCTGT
```

FIGURE 3A-4

12801 CATACATGTC ATTTAACATA ATGCTTATCA CATTGTATTG AAATGTATCT
12851 TATAGGTATT TTTTCTCTAC CAAACTTGAA TTCACTTTTC TCCTTTAGCC
12901 ATCCTGTACT GAGCAGTGTT TTGGGTCTGG CAAATAGTTT GTACTCAGTA
12951 AATGTTTGGA AAATGAGTTT TAACTGTTTT ATTTTCGTGG GGTGAATTCC
13001 TAGTAGCAAG GGTATTCAAA TTTTATTATC TACTTCTTCC ACCTGAACAG
13051 CTTCATCGTA ATTATACTTT AATTCCCTTC ATTCTAGGCA GGTAATGGAT
13101 AAGTTCCAAA ATTACGATGT TGTTGGAGAG GTTTGAATAT TACTAGCACA
13151 TGAAATCTGA TTTGAACTGA CTAAATGAAG GTTTAGTACA TCATTATGAA
13201 TTAGTGTGAA CTAAGTTTTG CTATGTTAAC TTCTCTGAAA TCTCAGTCGC
13251 ATAATGTGAG TGTCTTTCTG GCTCATGCTT CATGCCTGAG ACTAGTGGGG
13301 GTTGTGTCTG CCTATTAAAG TCACTCGGAC CCAGGTGGAT TGGAGATTCA
13351 TCTAAAGACA TGCTTCCCTT ATCTCTAAGG CAGGAAAAGG AAATGGGGCG
13401 CATCTCTCAT TGGCTTGTAA TGCTTCTGCC CAGAAGGAGC TGTCACTTCC
13451 ACTACGTTTC ATGGATCAAT TTAAGACTCA TAGACACACC TATTAGTATA
13501 TTCGAAGGAA GTTAGAAAGA GCAGTGCCCA GAAGAAAAGG GGAGTTTGTC
13551 AGTAGCCCTA ATGACTATCA CAGTTACTGA AAGTGTGCCT TGGGCATAAT
13601 CTATCTTAAC TCCCAGATAT ACGCTGACAG TTGTTTTTCT AAAAGTCATT
13651 CACAGTGCTC AGATTCTAGT TAGTCCAAAT TGATATGGTT TGGCTGTGTC
13701 CCCACCCAAA TATCACCTTG AGTTGTAATA ATTCCCATGT GTCAGGGGGC
13751 GGTGCCAGGT GTAGATAATT GAATTATGGG GGCGGTTCCC CCATACTGTT
13801 CTCTTGGTGG TGAATAAGTC TCACAAGATC AGATGGTTAT ATAAATGATA
13851 GTTCCCCTGC ACACGCTGTC TTGCCTGCTA CCATGTAAGA CAGGCCTTTG
13901 CTTCTCCTTT GCCTTCCTCC ATGATTGTGA GGCCTCCCCA GCCATGTGGA
13951 ACTGTGAGTC CATTAAACCT CTGTCTTTTA TAAATTACCC AGTCTCTGGT
14001 ATGTCTTTAT TAGCAGTGTG AGAACAGACT AATACAAAAT GTTATACTAA
14051 ATATTAATAT TTCATCCTCT GATTGGCCGT GATAATAGCA TCAACTATGC
14101 TAAATTTCTA ATAATACACA TATTTCTAAT AATATGCATC TAATAGGGTT
14151 TATATTGTGA TTATGTAAGA GAATATTCTT GTTCTTAAGA ACAAGGGTCC
14201 TTAATCTGTC ACAGGATTAG AGATTTAAAG AATAAGGATC TCGATTCTGC
14251 AGCTTATCCT CAAATGTTCA TTAATTATGT GTGAGTGTGG AGAGAGAGAA
14301 AGCAAACATG GCAAAATGCC ACTTTTCAGT TGGTGAATTC AATTGGTGAA
14351 TCTGGAAGAA GGATGTACAG GAGTTATTGT ATGATTCTTG CAACTTTTTT
14401 GTACATTTGA ATTTTTTTCA ATAGAAAGTT AAAAATAATC ATGGCACAGG
14451 TTTACAAAAC CCTTGTAAAC ATTAGTGTTA ACTACTTTTA AGCCATTATT
14501 GCTTTTCATT CTGATTGATG TTTTGAAAGT ACTTTTCTTT TCCTCTGAGG
14551 CCTGTAAAAT ACGTGGACTA TATTAATCAG TGATCTTTCA AAAACAAAGA
14601 CTGAGGCCCA AACATTAAAC CTAGATGGAA ATCTGATTTT TAAAAATTCA
14651 CAAATAATGC CAGATTTCAT TTAAAAGACT TTTTTTCCCC CTTCTAGTTG
14701 GTTGAAATGT TGGATATGTC TGTCCCTGCA GTTGCTAAAT TGAGACGTCT
14751 TTTAGATAGT CTTCCAAGGG AAGCTTTACC AGACATCTTG ACATCAATTA
14801 TCCGAACAAG CAACAAAGAG AAACTCCAGG TACAGTGTTC CCTTTTGAAC
14851 GCCAGGTTGC TTTGTCACTT TTTATTGAGA ACTAGATAGT GAGTAGTTAA
14901 GTTTTGACCT TCAAGAAAAA GATATTGGAG ACCCAAAGTA ATTGAAATGC
14951 TTTTACATTT AAACTGACTT TCAAATGTGA TTGTTTTATA TTTTTGTTGA
15001 CACAAGCAGC TCTTTTATTT TATATTTTTG TTGACACAAG CAGCTCTTTT
15051 ATTTGCATAA TCAGTAATGG TAGTCAATTT ACAGAAAAAG TTAAAGCAAA
15101 GAATCATAAA AAGGTAAATA TTTGACTGGG TGCTCACGCC TGTAGTCCCA
15151 GCACTTTGGG AGGCTGAGAT GGGTGGATCG CTTGAGATCA GGAGTTCGAG
15201 ACCAGCCTGG CCAACATGGT AAAACCCCAT CTCTACTAAA AATACAAAAT
15251 TAGCTGGGCG TGGTGGTGCG CGCCTATAAT CCCAGCTACT CGAGAGGCTG
15301 AGGCAGGAGA ATCGCTTGAA CCTGGGAGGC AGAGGCTGCA GTGAGCCAAG
15351 ATTGCACCAC TGCACTCCAG CCTGGGCAAC AGAGACTCTG CCTCTAAATA
15401 AATAAATAAA TAAATATTTA ATTTAACTTA AATAIGTAGA CATTCTTTGA
15451 TTCACTATTT TTAAACGTGG AGCCATGGCC CTTCCCTTAT GTGTGGACCT
15501 GCTTTCTTAG AATCTTCATC ATGTTTCTTA TATAAATCAC ACCTATGATG
15551 CATTACTTAT AATTTTAAAT TTATATTTAT TTAAAGTGAA ATGAATTTTA
15601 AAGACACTTG AAAAGTAATC CAAGTATAGA ATCCTACATT TACATGACTT
15651 AATCCCCAAA CTGTAAATACT TTAAGTTTTC TTGCACACTT ATTTTTAAGA
15701 TATTTTTAAA GCAGTATTTT TAATGAATCA TCCTAGAATA TTTGTTTGTT
15751 TTCAGTGAAA CAGCTCTTTC ATATGTTATC AGTTTATTTA ATACTTAAAT
15801 CCAACTGTTA TAATAGCAAA TACAACTAAC ACAAACAGGT TGGTTATACA
15851 CAGGAATTCA ATTAATCCAG TGGGAGTAGA AGAGTTACAG GACTGCCAGA
15901 GAGCCCCCTG GCTGTGGGCG GCAGCAGTGT GTTTTACTGC GGGAACAGAG
15951 AGCGGCCTGT GCTCCGACAA ATCACTAGTG AGAGTTGGTT GAGTGCTTCT

FIGURE 3A-5

16001 GTTCTCTTGT GTATGTAAAC ATTTAATATT TTGAACCTAT AATTTGTTTA
16051 GATCTAATAT GAAAACACAT TCTGGGCTTC AAGAGAGTAA TTCCCAGAAA
16101 GAGTTGACGT CAACTGTGTG TCTGGTTTTT TCATCTTAAA AACACACAGC
16151 TTCGGCCGGG CGCAGTGGCC CACGCCTGTA ATCCCAACAC TTTGGGAGGC
16201 CGAGGTGGGA AGATCACGAG GTCAGGAGAT CGAGACCATC CTGGCTAACA
16251 GAGTGAAACC CTGTCTCTAC TAAAAATACA AAAAATTAGC CGGGCATGGT
16301 GTGGGTGCC TGTAGTCCCA GTTACTCTGG AGGCTGAGGC AGGAGAATGA
16351 CGTGAACCCA GGAGGGGGAG CTTGCACTGA GCCAAGATCT CGCCACTGCA
16401 CTCCAACCTG GGGACAGAGC AAGATTCCGT CTCAAAAAAA AAAAGAAAAA
16451 AAAAAACCAC ACAGCTTCAT TTTAAAGTGA AAAACCAAGA TCCTGTTTTT
16501 TCTTTCTTTT TTAAGGATTC TGATATTCAT CTCAAACAAC CTTGCTGATT
16551 AATATAGTTC ATTTGGTTGT CTTAGCCATA GTGTAGCTTT GAATACTGTT
16601 AATAATTTTT TTTTAACTTG GCAATTTAAA CCATGGCTCT GACTGTCTGT
16651 TTTTGGATTG TGTGTTTCTG AGAGAGATCC TATTGATTGA CTCACATTTC
16701 CTTAGATTTT AGATGCTGTG AGCCTAGAGG AGCGGTTCAA GATGACTATA
16751 CCACTGCTTG TCAGACAAAT TGAAGGCCTG AAATTGCTTC AAAAAACCAG
16801 AAAACCCAAG CAAGATGATG ATAAGAGGGT AAATATTTAT TTTAACCCAT
16851 TTCAGTTTTG AAAAAAAAAT AAGGAGAATA AAGAGAGGAA CAAAGAAGAA
16901 AAGTTTATTG TCTCCTACCA CTCGCACTAC TGATAAAATT TAGGTGTTTC
16951 CCTCTCATCC TTTTCTTTGC CTGGATTTTT TTTTAAAGCA TGTAAGCATT
17001 TTTCTCACTT TGTTTTGGTT ATCATCCAAA AGGATAATTT ACTGAGCCAT
17051 TTCCCCTTTT GTGTTGTTTC CAATGTTTTG TGTATTGTAA ACACTAACAA
17101 ATAACTATGA TGGGTGTCTT TGAGTATAAC ATTTTTTTAC TGCATGTAAT
17151 ACTAAGAAAC TAATACAAAA CTCTTTCTTA AAAGGACTAT ATGTTGTGTC
17201 AAAATTTGGC TGTTTTCAAC TTATAATAAG TTTCCATTTT TATTTAGTCA
17251 AACTCTTGAT CTTTTTTTGT TTTCTAAGCT TAAGTCCTCT AACCTTCAGT
17301 GGCTTGATAA ATATTCACTT TCCTTTCAGT TTAATTTTAG TTGATTTTTT
17351 AAAAAGTATT TAATTCTTTA ACCCATATAT TATTTTGAAG ACAGCAGTTG
17401 TATTTTTCCC TCAAATAGCT TTTTGTTTGA CTCAACACCA CTAATTAAAT
17451 AATCCTTCCC ATCCCCATTA TCATCTATTA CATTTATATG TATGATGGGA
17501 TCTGTTTGAA GTCTACCTTG ATCTGCTGAT TTTACTATTT TTATGTCTGG
17551 ACAGAGTTTA TATTAGGAAG ATATATTTGA TGTGGACAGG ATGTGAAAAT
17601 GGCATTTCTC TGAAGGTGTT GAGATGCAGC GCTCTGACTT AAGTTGAGGC
17651 GTTGAGAATT ATGTTAGCAA TTTGACGTTC ATCAGCGCAG AAGTCTTGTC
17701 ATCAAAGAGA ATACATTGTA GAGAAAGCGG AGCAGAAGGG AAGAACTCCT
17751 CCCCGGTGGG ACTAGAGAAG GGGCAGTCAA GTAGGCTGAG GAGAGAGATA
17801 GGAACAGTGA TGATCATGCT GGCGATTAGT ACTCCAGGAC ACCATGCTGT
17851 TTAAAACATG CAGAAAGCTG GATTATTTCT GGCTTGAGAT CAGGTCAGGG
17901 ACTCAATTAC TCATTTTGTA TAGAGAGACA AATCCACTGG GAGTTGCAGA
17951 AAACTGCAAC TTACTCTCAG TAAAGTTTGC CATCACTTAA AATGAAAGTT
18001 TTTCAAAAGT GCTCCAGAAA ATAAGCAAGA GACAGTTATT TAAAAAGTAG
18051 GAATTAGGAT AATATTTGGA GTTAACCTAA AACTCTCTCC TTTTTGTTCC
18101 CCTAAGAGTT GAAAAGCACT GTTTTAGCAG TCAGGAAGGA AAAATGCATT
18151 AAAAAGTGCT TTTGTCTTAA CAATGAAATC ACTGATATGC TTATAAAAAT
18201 CTCACTTTTA AAAAATATAT AATATGTTCA GTTTTTTATT TATAATATTT
18251 TATCTGCTGA TGACTTATGT AAGAATAAAA GCATATATTT AGTACTTGTG
18301 TTTTTATAAA ATTAAATTTT TATTTACTGC TTTATGTTTT AAACATTTTT
18351 ATATTTGAAT GTATTAAATA GATAAATTTT CCAGGTTAAA AAATAAGTTC
18401 TGGGCTGAAT GCAGTGGCTC ATGCCTGTAA TCCCAGCACT TTGGGAGGCC
18451 AAGGAAGGAG AATTGCTTGA GGCCAGGAGT TCAAGACCAG GCTGGGCAAC
18501 ATAGTGAGAC CTCATCTTTA CAAAAAAAAT TTAAAAAATT AGCCAGCATG
18551 CTGGTGTGTG TCTGTAGTCC CAGCTATTTA GGAAGCTGAG GTGGAAGGAT
18601 TACTTGAGCC AGGGAGGTTG AGGCTGCAGT AAGCAGTGTT CATGCCATTG
18651 CACTTCAGCC TGGATTACAA AGCTTGACCT TGTCTCAAAA AATAAAATGT
18701 TCTGGGGGCT TTTAAATTAA ATGCTAGTAT ATAATTTTGC TCCAGTAGTG
18751 GTTGTTTATT CATGAATTTC AAGGAGCATA TAAGGTAGTT TTAACATATG
18801 ATAGAGAGAT CATAGAGAAT ACAAAGGCCA TTTGACTTTG CACAGAATAT
18851 GTTTTTTAGA TTTGAAAGAA CAATTTTGGC AGGATGGGAA CAGATGCCGA
18901 AGGCTCACTG AAGTAATTGA TGAGGTAGGG GATCTGGTGG TTATAGCCAC
18951 TTGCTGGAGA AGCAGAACTT CACAAGAAAG GAAGTAAATA GTGCGATAGT
19001 TAACTAGAAG AAACTAGAGG TAAGAAAAAA ATATTTTGAA AGCAGGAAAG
19051 CTTTGAAGAC AAAATAGAGC CAGTGGTGGA AAGGTTGAAG ATGCTAGGAA
19101 GAAATTTTGT AATGTAGGAG ATAAAATGGA ATTTTTTTCA GTCACCAAAT
19151 GGTAAGAAGT AATGTATTTC AAGAAAATAG TGGCTGCAAT AGTAGCTCAA

FIGURE 3A-6

19201 AGAAAGGTAA TTCCTAGATG GTTTAATTAT TTCTAGTATC CAGTTCCTTG
19251 AAATTTGTTT TCTCATGCAA GTATTATTGT AAGCATATAC CAAAGAATCA
19301 TGTCTACCTT ACGTTGGTCT ACTTCTGCAA TTCTGCTGCC TCTCTGTATA
19351 CAACTGCCTT TTGATTATCA TTCTGAACTT CACTTCCTAA AGATAGAGAC
19401 TGTAGTCATA AAAATATTTA TTCAGCACCA GTCATAATCT TATGTGTACC
19451 TGGGTACTTC GTTTCCAATT TATTTTGACA TACGGTTTTA CTTTTCTGCT
19501 TTCTATGTTA GGTTATAGCA ATACGCCCTA TTAGGAGAAT TACACATATC
19551 TCAGGTACTT TAGAAGATGA AGATGAAGAT GAAGATAATG ATGACATTGT
19601 CATGCTAGAG AAAAAAATAC GAACATCTAG TATGCCAGAG CAGGCCCATA
19651 AAGTCTGTGT CAAAGAGATA AAGAGGTAAA TTATAAAAGG CATTTGTTCA
19701 TTATTGTTTT CATTCTTGGT ACTCCTGATT AACACCACTT TCACTACTCT
19751 TTTCTCCAAT ACTGAGGATA CATAATACAA ATCTTCCACC TGCAGTGTGC
19801 TGTCAGGCAA TATAACTCTT GCAGCTGCCT TTTTGTTGTC TGAAAGAACA
19851 GACCATGCTT CTTTGTTTAT ACGTAATGTT TGTTCAGTTA GCATCATATT
19901 CTTCACATGT GACTTTTCTT CTCTAGATTA TAAACTCTCA AGGGCAAGGA
19951 CTGTCCATTT CTCTTTGTAC AAGACAAAGT ACAGGGAAAC CTTGATAACA
20001 GAATAGGATA TATGGGTTGA TTACATTTTC TGGATATCCC CAGTGTTAAA
20051 CTGAAAGCCA TTTTTCCTTT GCATACTTTT AACTTTATAA CTCTTATTAC
20101 ATTTTCTTTT ATTAGTGAAT TGTAGTGAGC CTGCTTGAAT GCTTAGTGAC
20151 TTAATATTTG ACTTTCTGAG GCTTACAGTT AAGAACATTA GTAATTGTAG
20201 TTGATGGGTA TTTTATATTG CCTCTGACAT TAGTTAATAT ATGTAGAACA
20251 TTTATTATGT GCAGAACACT TTGCTAAGCA TTGCATATAT TATGGAAGTA
20301 GCATTTGTTA TTAAATATAT GATATTAGCT TGCTTTTATG AGCAGACCTC
20351 ACTCATCTCT GATACAAAAA AAAATGTATT GTATTATGCA TAGTTAGGCA
20401 CTTACATCTT ATTGTGATAA GTAAACCAAT GGATATATGT CACTTGACTA
20451 TCCCTGTGAG CTTAAAAGGG ACACACACTA GTAAGGCCAT ATTTCCAGGT
20501 TAGAATTAGA TATAATGTTT TCTCCTGCAG TTTGCAGGTA TCTGCCTTAT
20551 TTTGTTTTGT AAGTACCTTA AGTACTTAGA AAATATGAGA ATACTTTGTA
20601 GAGAAAGCAG AGCAGAAGGG AAGAACCCCT CCCTGGTGGG ACTCCAGAAG
20651 GGGCAGTTAA GTAGGCTGGG GAGAGAGATA GGAGTGGTGA TCATTACATT
20701 ACAAAACAAA ATAAACGTTT TATTATCTGG ATACTTTAAA ACTTTTTCAG
20751 ATTTGTTTAA ACATGCATGA TATATCTAAC CAAGAAAGAG AGCTGTGTTT
20801 GATTTTTCTG TTATGGAATT TTTCTGTGTT CTTGAACATG TTTGCTGTGT
20851 ATTCTTTCTC CACAGACTCA AAAAAATGCC TCAGTCAATG CCAGAATATG
20901 CTCTGACTAG AAATTATTTG GAACTTATGG TAGAACTTCC TTGGAACAAA
20951 AGTACAACTG GTAAGCCAAA AAATAACACC TGTTTTGCAG TCTAATTGTC
21001 ACTCAGAAAG CTCATGCAAT TTTTCATTTC AAATTTACTC CACTGATTGT
21051 CGTACTGTTA AATTATTTTT GTTTTCAATT TTTTTGAAAC CATTTTATTG
21101 AAGTGTGATT GTCGTACAAA AAGCTGTATA TAATTAATGA ATACATCTCA
21151 GTGAGTTTCA GAATAAGTAT ACACCCATGA AACCATCACA ATCTTCATAG
21201 CCATAAACAT ATCCGTCACC TCCAAAGTTT CCTCCTACCT CTTTTGTGAT
21251 TATTATTATC ATCATTATTA TTGGCTTTTT TCTTTTGGTG CTGGTGGTAA
21301 GAACATTGAA CATAAGGTCT AATGTTAAAT TAACAATATT GTTAGCGATA
21351 GGCACTTTTC TTTATAGTAG ATCTCTAGAA CTTATTTATC TTGCATAAGT
21401 GAAACTTTGT TCCCTTTAAC CATCACCTCC CATTTCCTTC TCCTCTCATC
21451 CTGTGGCAAC TACTAGTCTA CTCTCCATTT CTATGAGTTT CACTATTTTA
21501 GATTCCACAT GCATTAAATA GGTGAAATCA TACAGTACTT GTCTTTCTGT
21551 GTCTGGCTTA TTTCACTTAG CATGATGCCC TCTAACCTAG AGGTCCATCC
21601 ATGTTGTCAC AGATGGCAAG ATTTCCTTCT TTTTTAAGGT GCATAATATT
21651 CCATTGTGTG TCTATACCAC ATTTTCTTTA TTCACTTATG TGTCAGTAGA
21701 CATTTCAGTT ATTTCCGTAT CTTGGCTATT GTAAGTAATA CTGCAGTGAA
21751 TACGGAAGTG CAGATAACTC TTTGAGATCC TGATTTCAGT TCCTTTGGCT
21801 GTTTACCCAG AGGTGGCATT GCTGGATCAT ATGTAAGTTG TATTTGAACT
21851 TTTTTAGTAA CTTCCATACT GTTTTCATAA TGGCTGTTAT CGGGGACCT
21901 GCCCCAATAA TCATGTAGGT TCTTTTCTAT TTTCCTAAGC ATTGGCTGGC
21951 TTGAGAAATA AAGAGACAGA GTACAAAAGA GAGAAATTTT AAAGCTGGGT
22001 GTCTGGGGGA GACATCACAC GTTGGTAGGA TCCGTGATGC CCCACAAGCC
22051 ACAAAAACCA GCAAGTTTTT ATTAGGGATT TTCAAAAGGG GAGGGAGTGT
22101 GCGAATAGGT GTGGGTGACA GACATCAAGT ACTTAACAGG GTAATAGAAT
22151 ATCACAAGGC AAATGGAGGC AGGGCGAGAT CACAGGACCA CAGCTCCGAG
22201 GCGAAATTAA AATTGCTAAT GAAGTTTCGG GCACCATTGT CACTGATAAC
22251 ATCTTATCAG GAGACGGGGT TTTGAGATAA CGGATCTGAC CAAAATTTAT
22301 TAGATGGGAA TTTCCTCTTC CTAATAAGCC TGGGAGCGCT ATGGGAGACT
22351 GGAGTCTATC TCACCTCTGC AATCTCGACC ATAAGAGACA GGTACGCCCC

FIGURE 3A-7

22401 GGGGGGGCCA GTTCAGAGAC CTACCCCTAG GTGCGCATTC TGTTTCTCAG
22451 GGACATTCCA TGCTGAGAAA AAAGAATTCA GCGATATTTC TTCCATTTGC
22501 TTTTGAAAGA AGAGAAATAT GGCTCTGTTC TGCCCGGCTC ACCAGCGGTC
22551 AGAGTTTAAG GTTATCTCTC TTATTCCCTG AACAATTGCT GTTATCCTGT
22601 TCTTTTTCCA CGGTGCTCAG ATTTCATATT GCACAAACAC ACATGCTGTA
22651 CAATTTGTGC AGTTAACGCA ATTATCACAT AGTCCTGAGG CCACATACAT
22701 CCTCCTTGGC TGACAGGATT AAGAGATTAA AGTAAAGACA GGCATAGGAA
22751 ATCACAAGAG TATTGATTGA GGAAGTGATA AGTGTCCATG AAATCTTTAC
22801 GATTTATGTT TAGAGATTGC AGTAAAGACA GGCATAAGAA ATTACAAAAG
22851 TATTAATTTG GGGAACTAAT AAATGTCCAT AAAATCTTCA CAATCCACGT
22901 TCTTCTGCCA TGGCTTCAGC CGGTCCCTCC GTTTGGGGTC CCTGACTTCC
22951 CGCAACACGC TGTACCAATT TACATTCCGA ACAACAGTGT ACAAGGGTGC
23001 CCTTTTCTCC ATATCCTCAC CTTCACTGAT GATGGTTTTT TTGTTTGTTT
23051 GTTTGTTTTT TTAAATAATG GCCATCCTAA CAGGCATAAA GTGCTTTCTC
23101 ATTGTGGTTT TGATTTGCAT TTCCCTGATG ATTAGTCATG ATAAGCACCT
23151 ATTTGATTTT TTGCCGTTAA GTTTCATGAG TTCCTTGTGT ATTTTGGATA
23201 TTAACCCCTT ATCAGAAATA TGGTTTGCAC ATATTTTCTG CTGTTACATA
23251 GGTTGCCTTC TCATTTTGCT GAACTTTTTT TATTCTGTAC AGAAGCTTTT
23301 CAGTTTGATA TAATTTCACT TGTTCATTTT TGCTTTTGTT GCCTTGACTT
23351 TGGTGTCAAT ATCCAAAAAT ACCATGCCCA GACCAATGTC AAGGAGCTTT
23401 TAAAATATAT TTTGTTCTAG GAGTTTTACA GTTTCAGGCC TTACATTTAA
23451 GTCTTTAATC CATTTTGAAT TAATGTTTGT ACATGGTGTC ATATAAGGGT
23501 TCAAGTGCAT TCTTCTGCCT GTGGGTATCT GGTTTTCCCA CAACATTTTC
23551 TTGAAGAGAC TGCCCTTTCC CTATTGTATA TTCTTGGTGC CCTTGTTGAA
23601 AATTGGTTGA CCTTCTAGGT AACTTTATAG GTTTATTTCT GGGCCCTCTA
23651 TTCTATTCCA TTGGTCCGTG TGTCTGTTTT TGTGCCAGAA TCATACTCTC
23701 TGATTACTGT AGCTTCGTAA TATAACTTGA AGTCAGAAAG TCTGGTGCCT
23751 CCACGTTTGT TCTTGCTCAA GATTGGTTTG GCTATTCAGG GTCTTTTGTA
23801 ATTTCTTATT AATTTTAGGA TTTTTAAATC TATTTTTGTG AAAAATGTCA
23851 TTGGAATTTT AATAGGGATT ACATTGAACT TGTAAATTGC TTTGAGTGGT
23901 ATAGACATTT TAACAACATT CTTCTAGTCT ACGAACATGT AATATCTTTC
23951 CATTTATTTG TGTCTGACTT ATTTCATCAG TGTTTTATAA TTTTTAGTGT
24001 ACAGACATTT TACCTCCTTG GTTAAGTTTG TACTTAAGTA TTTCATTCTT
24051 TCTGAAACTA TTGTAAATGA GATTGTTTCC TTAATTTCTA TTTATTTATT
24101 TATTTTTTTG ACAGGAGTTT CACTCTTGTC GCCCAGGCTG GAGTGCAGTG
24151 GCATGATCTT GGCTCACTGC AACCTCTGCC TCCCAAGTTC AAGCGATTCT
24201 CCTGCCTCAG CCTCACGAGT AGCCTTAAAT ACAGGCACCT GCCATGACAC
24251 CCGGCTAATT TTTTGTATTT TTAGCAGAGA CGGGGTTTCA CCATGTTGGA
24301 CAGGCTAGTC TCGAACTCTT GACCTCAAGT GATCCACCTG CCTCGGCCTC
24351 CCAAAGTGCT GGGATTACAA ACGTGAGCCA CTGCGTCTGG CCCTTAATTT
24401 CTCTTTGGAG AAAGGTTTTT TTTTTTTTG AGCTTTATTG AAGTGTAATT
24451 GACGTACAGT AAACTTCACA AATGTAGTAT GTACATTTTG ATGAGTTTTG
24501 ACTTACATAT ACATCTGTAA TACCATCACC ATAATTAAGA TAATGAGCAT
24551 AACCCTCACC TCCAAAAGTT TCTTCATGCT CTTTGATAAT CCCTTCCTTC
24601 TTCCCCGCCC CTTTCCTCCT TGCCTCCTAA TCCCCAAGCA ACCACTAAAG
24651 ATTAATCTGT ATTTTCTAAA ATTTCATATA AATGGAATCA TAGAGTATGA
24701 GCCCTTTTTT CTGGCTTCTT TAATTCAGCA TGATTATTTT GAGGTTCATC
24751 CATGTTGCTG TATATAACAG TAATTTGTTT CTTTTTATTG CTGGAGTTGT
24801 ATTCTGTTGT ATGGATATAC CATCATTTGT TTATCAATTC ATCTGTTGAT
24851 AGACATTTGG GTTGTTTTCA GTTTTTTGGC TATTAAAAAT AAAGCTGTCT
24901 GGGCACAGTG GCTCATACCT GTAATCCTAG CACTTTGAGA GACCAAAGTG
24951 GACAGATCAT TTGAGCCCAG GAGTTTGAGA CCAGCATGAG TAACACAGGA
25001 AGACCCCAAC TCTATTTAAA AAAATAAAAT AATAAATGAA ATAAAAATAT
25051 TTAATAAAAT ATCAAAAAAT AAAGCTACTG TGAACTGTGG TAGTAAATTT
25101 ATTTTTAAAT TTATGTAATG TTTGCATGTC GTGACAAAAT ACTGCCTTTT
25151 AGTTGAAAGG AAACATTTCT TGGTACTCTG AGATGCCATG TGTGTCAGCA
25201 CTAGAGATGT GTAGCAGCCA TGTATCCATC ATGAAAATAA TTCCATTGTT
25251 TAGCATTGCA CATAGCACAA AGAACTGAAG ATGAATAAAT TATGGTATAA
25301 AAGGAGTCAT GTTAAGCTCC TAAACCATTA CTACACAGGA TTATGTCTAG
25351 ATAATTGTGA GTGTGGTTAT AAAACCATGA AAATGCCATT CATATATATA
25401 TTTTTGAGAT GGAGTCTCGC TCTGTCACCC AGTCTGGAGT GCAGTGGTGT
25451 GATCTTGACT CACTGCAGCC TCCGCCTCCT GGGTTCAAGC AATTCTCCTG
25501 CCTCAGCCTC TCAAGTAGCT GGGATTACAG GCGCTTGCAA CCACACCCAA
25551 CTCATTTTTG TATTTTTAGT AGAGACAGGG TTTCACTACA TTGGCCAGGC

FIGURE 3A-8

25601 TGGTCTCGAA CTTCTGGCCT CAAGTGATCT GCCTGCTTTG TCCTCCAAAA
25651 GTGCTGGGAT TACAGACCTG AGCCACTGTG TCCAGCCTAA ATATCTTTGT
25701 TTGTTTGTTT GTTCGTTTTT TGAGATGGTG TCTTGCCCTG TCGCCAGGC
25751 TGTAGTGCAG TGGTGTGATC TCAGCTCACT GCAACCCCTG CCTCCTGTGT
25801 TCAAGTGACT CTCCTGCCCT AGTCTACTGA GTAGCAGGGA TTACAGGCGC
25851 CTGCCACCAT GCCCAGCTAA TTTTTGTGTT TTTAGTAGAG ATGGGGTTTC
25901 ACCATGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAAG TGATCCTCCC
25951 ACCTCGGCCT CCCAAAGTGT TGGGATTACA GGTGTGAGCC ACCGAGCCTG
26001 GCCCCCCATT CATAATTTCT GAAAGAGAAG TTTACCTACC AAGTAGAGAT
26051 CTCAGATAGT AACCGAAAAC AAAAAGGAAA GCAGAGAGGA AAGAGTTGTA
26101 GGAAATATGT TTGCAGATTT TCCCAGCTTA GAGGAGTCAG TAGATACCAT
26151 TTCAATCTTC TAATTATAAA TAAGGAAATT TATATTGAAA TTTGAAAAAT
26201 TTTTTACATG TAATCACATG TTATTCAAAA CAGGAAGCAT GCTTTCTGAA
26251 TCATTAAAGA GAATAATTAG AAAAATATAT CCTGTATAGA AAAGATAGAA
26301 AATAATTTAT ACAGCATGGA AATCACCTTT ACTTAAAAGA TTGAAAGAAC
26351 TTTTAAAATT GTCTTTACTT GGCATATTTC TTGCAAGAAA TTTCTTCACA
26401 GTGTTTTCAG TCTTTTCTAA ATTATCTTGA CTTTTATTCT TACCTTACTG
26451 AATGTGTTAA TCATGAATGG ATAACGCATT ATAACAAGTA CCTTTTTAGG
26501 TACAAGATGA TATTTTGATG GAAACTTACT CTTCTTGAAC ATGATGACAT
26551 TGATGACCTA ACACTGAACC ATGTTTGCAT AACTAAAATA AATCCCACTG
26601 GGACTTAGTA TATTATTCTT TATAGATTTG ATTTACTAGC ATTTTAATAT
26651 TTACAGCTAT ATAAAAAGAT TTGTCTGAGG TTTTCTTTTA TGTTTACTGT
26701 GGTAGGTTTT AGTGTCAGGG CTAGCACTGT GAAACAATTG AGAAACTCTC
26751 TATCTTTCAC TTCTTCATAT ATTCATTGGT TGGGTTCTGG AGCCAGGAAA
26801 GGGGGAAGAA ATTTTAGTTG TTCTTCTCCT ACTTCACTCA CCTAGGACTC
26851 TGACTAAAAT CAATAGTACT ATAATTAAAT TATATAGTTT ACTGCTTAGC
26901 TAGGTTTTTT GGGGGACTAG CTTGGGAACC AAATTACCAT CTCAGGCCAT
26951 TTTTTTCCTT TATGAAATAT CCTTAGCAAA TTCTAAATAA TTAATTAAAA
27001 GATATGTATT AATTAATTAA AAGATTTCTG TGTATTTCTC TCTCCCATCT
27051 TCTTCTTTCA CTGCCAGCAT GATCAGGTGG CTGTGTATTA TACCCTGGCA
27101 GCCACCCAGC TAGTGAATTC ATTTTGGCTT CTGTTACCTG GTGTTTAATC
27151 TGAGTATTTT AAATGCTAAA TCTTATTAGT AAACCTGTTG AAAGCTTGGC
27201 TCTAGAAACA AAGCCTAACT CATACACTTC TGGTGAGACT TTGATACAAC
27251 TTTCTGTGTG GCAATTAGGC AATTCTTTAC ATCATCTGTT TTTTTTTTT
27301 TTTTTGACCC AGCACTTCTG TTCATAGAAG ATAAGCTGAA AGAAATCATT
27351 GCAGATATAT GGGAAGATTT AGTTCCAGTG ATGCACAGTT GAAGCATCTT
27401 TTATAAATGT AAAGATGTGT AAACAACTTG AATGCTCAGC AGTAGGGAAT
27451 TAGTTAAATG AATATAGATA ATTTAGTAAT GGAACATTAA GTAACCATAG
27501 AATGTTACTG ATAAATATAT GTGTGACAGT GAAAGTTGTC TGTCATATAT
27551 TAAGTGAAAA AAACATTTTA CAAAACTTAA AGGCCCCATA AAATCCCATT
27601 TTGAAAAATA GGTTTGTAAA TGCACGCACA CAGCCTGGAA TTACACATAC
27651 TGAAGTAAAG GTAGTGGTGA TCTCTTGGGG GCATGAGATT ATGGGTAACT
27701 GTTTTCTTCT TTTCTGTTAG TGTTATCAGG TTTTCTGGAA TGAACATATG
27751 TTACTACTGA AATAAGGAAA AAAATCACCC TTTTTTTTAA AAAACAAATG
27801 CCAGCACACA TACAATATGT AGAAATTAAG AAGTAATGCA TAACTAGAAA
27851 ATCATTCCAA ATAAAATGAT ATGAACATTG AGTTTTTAAT TGTGTAGTGC
27901 CTACTATCTC TGGGGACACT AAGTCTTAAG CAGAGAAACC AAACCAAATG
27951 CAGATCTCCT AGAATCCTCA TCTAGAAAGA TCCAAGTCTG TTCTTATCAC
28001 ATCTATTTTC AAAAAAAATA TTTTGCCCTC GTCATGCTTG AAAGGAGTTC
28051 TTTAACTTAA AAATTTTATG TGTTCTAATT ATTTCTGTTG GGTTATTTGA
28101 CAGACCGCCT GGACATTAGG GCAGCCCGGA TTCTTCTGGA TAATGACCAT
28151 TACGCCATGG AAAAATTGAA GAAAAGAGTA CTGGAATACT TGGCTGTCAG
28201 ACAGCTCAAA AATAACCTGA AGGGCCCAAT CCTATGCTTT GTTGGCCCTC
28251 CTGGAGTTGG TAAAACAAGT GTGGGAAGAT CAGTGGCCAA GACTCTAGGT
28301 CGAGAGTTCC ACAGGATTGC ACTTGGAGGA GTATGTGATC AGTCTGACAT
28351 TCGAGGACAC AGGTAGAACA CTTCTCTCAG TTTAATCTCT GATTCCTCTT
28401 TCTTTTTAAT TGACTAGAGC TCCCTAAAAG CTTAGGCATA GCATACATCT
28451 ATTTTCCTTA AAGGGCTATG TGTGGTACCT TGAATGAAAA GGACATTTAC
28501 AAGAAGTATC AGCTAGCCTA GAGCCTCTAA GCGTAATGAT AAACCCAAAC
28551 TAACCTTGAT TTGTATGACA GTGGATACTA CTCTGTGCCT CAACTTTCCT
28601 GGAATCTCAT TTGAATGTAA TTATAAGTTA TTTATGATTG GATATTATTA
28651 TGTCTTTACA CTCTTTTCAA CCCAGTAGCA TGCCATAAAT AATGATCCCT
28701 AACTCTCAGA GTTAAAAAAA GTAACTGCAA TAGGGAGGGC CAATAGGAGG
28751 AGGTGAGAAG TCTTTGATAA CAAACTTGTT CTGATTGCAG TCTAAACTTC

FIGURE 3A-9

28801 CTCTTATGAA GGTTGGTTTG TATTATGAAT ATGAGTAATA AGGATAAATG
28851 TTAGCATAAT TATTAAGGCT TATTCTTGCA TTTTGGACTC ACTTTCTATA
28901 AAAAAACAAT AAACTGTAAG AACTGTCCCT CTAGGCTGGG CACAGTGGCT
28951 CATGCCTGTA ATCCTAACAC TTTGGGAGGC TGAGGTGGGT GGATTGTTTG
29001 AGCCTAACAG TTTGAGACCA GCCGGGGCAA CATAGGGAAA CACTTTTGTC
29051 TCTACAAAAT TTATATTTAA ATTTTTTAAT TTTAAATTTT AATTTTTGTC
29101 TCCACAAAAA TTAAAAAATT ATGCAGGCAC AGTGGCATGC ACCTGTGGTC
29151 CCAGCTACTC AGGAGGCTGA GATGGGAGAA TCATTTAGGC CNNNNNNNNN
29201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NAACCAAGCG
29251 GCAAATAAGG AAACTTTGTC TTACACAAGT AAATTTACTT CTTCATTTAC
29301 ATTAAATTTG GTTCCACAAA AATATAAAAT TAAGCTAGGC ACAATGGCAG
29351 GCCTTGTGTT CCCAGCTCTT AGAAGGTCTA AATGGAGTAT CATTACGTCT
29401 TGAAAGTTCC AGTTTGCAGT AACCCATATT GTCCCCTCGC ACGCCAGCCT
29451 GGAGACAGAG ACATTATCTC AAACAAACAA ACAAACAAAC AACAACAAAA
29501 CTGTTTCTGA TTAATCTGAC ATTATTAGAA TCAGATTTGC ATGTTGCATT
29551 CATTGTTCTC ACTGGTCTCT TTGTTGATCT GATGGAAATT GCCTTGGGAA
29601 AGCATGAATT TACATTTCGT GGTTTAAGGG ATTCATAGCA ATTGTAAGTT
29651 GTGAGAAAAC ATACCTATAG TGTATGTGTT AAAGAACATG TTTAAATGTA
29701 GGAACCATGA ACTGCTTATA AAAGAATATG ATGCTTTTTT AATATCTTGT
29751 TTTCTATTTG CCTTATTCAA AGGGATCCCT ATCCATAGAC AGGGATGGGA
29801 AACTGTTTCA GAAACTTTTC TATAAGAAAT GGTTATTTTT ATTCTCTTTT
29851 ATTTGCTCAC TTAAAATTCT TACGCATTTA AAAAGTATCA TTACTGGCCT
29901 TGTGTAGTAG CTCATGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGGCAG
29951 GCAGTTGCTT GAGCTCAGGA GTTCAAGAAC AGCCTGGGCA ACTTGGTGAC
30001 ACCCCATCTC TAAAAAAATA ATAATAATAA ATTTTAAAAA AGACTCATCA
30051 CAAGATTTTA GTAAATAAAC AATGAGGCGT GCAGATCAGA GTAGAGAATT
30101 GATTTGGGTG ATTTCTTCTG GCAATTTCAA AAGATATTTT TGTTGCCTAG
30151 ACTTCTTATT CTTGCATGTA CCACTAGAGG CTATAGTTTG CTTTCGTAAA
30201 GGAATTGGCA TTTCTCTTGG ACCAAACTCA AAGAAGCTGC GTCTAGGGCC
30251 TAAATCTTCT AATTTTAGCT ACAGAGTAAG TATTTGATGG CATTTAGAGA
30301 GTGAGTTCGT GGAATTAATG CTATGTGAAA TTGACATCAT AAGCACGTGA
30351 CATGTAGGTA ATTTGTTCTT ATTTCTTTTC ACATTGGTAT TGATTATTTG
30401 ATAAGGCTTG GAAAGCACTT ATTCAATACC TGACACACAG TGAGCATTCA
30451 CTAAAAATTA GCTTTAACCA TTATTTAAAT TCTATTAATA AATTCTCAGG
30501 AGGACAAATT TAGATTTACA AGCTTCAGTA TGAGTTTTTA TAAATTTCAA
30551 TCTGATTTTT TAATTGCCTT CTAAAATATT TATCCTATTC TCAGCATTAT
30601 TACTTAATTT ATACGGCAGA ATTATGGGAA AATGCATTTT TCTGTTGCCT
30651 ACTAATGGAC AGTGTATAGT GTCATGGTTC TCACCACTTA CAAACATCAC
30701 TGGATTAAAA TAAATCTCTA TTTTAAATCC TTACTGACAT ATAAAATTTG
30751 TTCTTTTTTT CAAGTGAATA TGCTTTTGTG TATGTGACTG TATTAAGAAA
30801 ATTGAGTCTG AAGAAAATAA GAATTGACTT TATGGGTCTT TTGTAAAAGG
30851 AGGTTGTGTT ACAATCACCA TTGCCTAAAA TATTTGTAAA TATAACCTTT
30901 TTAGAAACGT ATATATGGAG GCTGTGATTG TTGCCGAGTA AAAAGTATAA
30951 GGATTTGTTT TGTGAATCAT TCTATTCAGC CTGATTTTAG ATACACCTTG
31001 CTGGTAAGTG TTACTTAGCC ATCAGTGTAC CAGATGTTTG ATTAACTACT
31051 ATAGCAACCT GCCCTTGTGC TGTTGGGGAC ATATTACCCA TCTACCCCGT
31101 GAATTATTAA AGCCTGGTGA AAAATTTTAT TTCAAACCCT GTTTGGAAGC
31151 ACGTGGAGAG TAGTGGGGTT CAGTTGTTGA GGAAAGGGTG AGGGCAGAGC
31201 ATGCACTTAG GTCAGTTATG AATTGAAGGT GAATAGGAGG AGGAGAGAAA
31251 GAACAACCGA CAATTCCAGC ACAACCATGG GTGTGCCTGG GGGAACATGT
31301 GGTTCCATGT GACAGTTGAG GCATTTGGGA GACAACCCAG GTCTTGACGT
31351 TTGAGTACCG GTCACATGCT CACAGTTAGA GTTCATGAAA AGTTTTGTTT
31401 TTCCTCAGCC TTTGAGTAGG CACCACTGTT CCGCAGCCTT AGAATAGCCA
31451 AGGAAAAAGA AAGCCAGGGA AAAAGAAAGC TGCTTTGTTA TTGTCCTTGC
31501 TTATCCTCTC GATTTTGCCA CTCACTCTCC CTGTTTTCCC ATGTGTGGAA
31551 CACTTTCCTT TTGCTAAAAG TACCTGCGTA TGAGAAGAAG GATGCCGATA
31601 AGTTGGGGAT TGATTTTAAA AACAAGCAAA GATATGTTTT TTATGGTTAA
31651 ATGATAATGA GGTGGGAGAT GGGGAAGCAA AAGAGAGGCT TGCCTTAATA
31701 TTTAATCTTA AACTTGGAAA ATAATAGTGA TCTGACTAAA CATTGCCTCA
31751 TTTTTGTCTG TATTGTTTTG AGTAGCTTAA AGGAAGAATA ATGTTTATGC
31801 TACGTATTAA CTCATTCAGT TTTTCAGTCT TTTCGATATT TCTCATTTGG
31851 ATTTATCTCC ATTGTGATTT TTCTGTCCAC TTTGTAAGCC ACAAAATACT
31901 CATTCCCTTC TATCAGTTTT AACAACTTAA ATTTTTATAT TTAAGTATTA
31951 CATTTAAATA ATTTAAGTCA ATTCACACAA ATATAAGGTA ACTAACTTCT

FIGURE 3A-10

32001 TTTAAGATGA AGTTTTATGA AATAATGTTT GCATAATTGT TTTTCATTTG
32051 TTCTTTGGTA AAAAGAAATA ATATATTATT GTTATGATAT ATCTTAAATC
32101 ACTGTGGATA TTAACTCCTA GAAATACTTT ACCAGCTGTT TACTTAGATA
32151 ATAAAATTAT ATTATTGCAA GAAATCCTTG TCTCAACTTT CAAACAAGAT
32201 GAGAAGAAAA ATGAACTTGT GATTTCCACA TTGATACATT TTCATATGCA
32251 ACCTGAAATG GTAAAGTTAT AAATAAACTA TTTCATTATT AGTTTCTACA
32301 AGGGAAAAAT AACTGAAGCA GCAAGCTTCT AATGTATTTT TTTAGCATAG
32351 TGTACCAGAT ATATTATGGT TTGCCCACTA TCCTTTCAAC TTACATTTGC
32401 ATGTAGCTCT TCTTTGCCTC TCCAAAACTT AGGTTTATTT TAAGGCCTCA
32451 ACCCAAGGCT TCCTCCATTA ATGTAAGTGC AGTCAGTTAT GATTTCACTC
32501 TTCTCTAAAC TGACCACCTA TTGTGCTCCT TTATCGAATA CGGGCCTCTG
32551 GCATTTCTAC CATACAACTG TGGAGATGAA ACATAAATAC GTTTATAAAA
32601 AGTACAAGCT TTCTCAGGCA GGGGATTTAT CGTCTATCTC CTTTATGTAC
32651 CCCATGATGC TTATTTAACA TGGTGCTAAA TGTGGTGAGC GCTCTCTGGG
32701 TGTTTTGTGA ATTCATGTAA GATTAAAACA TAATATTTTG GAAGTTATGC
32751 AACCCTTTAG ACGAGTACAC CCATACAAAT TAGTCTATAA AAAGATTTAG
32801 GAATGACTAC CAGAAGAATA ATTGCATTTG TTTAGACATG CTATTATACA
32851 TTAAAATCCC AGTTTCTTAA AGACTGTTTT TCTTTTTGAG ATCATTAGGA
32901 TCTTTTTTAA ACTGATTCCT TTTTCCAGTT TGAGATACAC ACACACACCC
32951 ACACACCCAC CCACACCCAC ACCCACACAT CCACACACCC TTGGTAGAAA
33001 ATGTGAAAAA TAAGGGGAAA AAATCCTCAT GTTTTTCTAC CGTACAAAGA
33051 TAATCACTGT TAACATTTGT TTTGTTCTGC CAGACTTATC ATTGGATTTT
33101 AAGTAACAGA ATTGTAATCC TGTCATTTTC ACTTAACATT GTAACACTTA
33151 AACTCTTTTC TATTCCAAAT TCTTTGTAAA TTTTATTTTA ACAGTTTGCA
33201 TTATAGCCTG CGGGAGCCGA GCCCTTTAAT TGAATAGGTA GGAAGAGTGG
33251 ATGGTGAAAT GCCTATATTT TTCTCTCTTG TCTGCTATAA AAGACATTTG
33301 CAAAAGTTGC TTCCATGAGG CAGAAATTGA AATGGGACTC AAATTCAGGT
33351 GTACTGAATT CTGCTCTTGT GCTTTTTCCA GGAAACCAGA AGTAAACTTT
33401 AAGTAGCTGT TGCTAATAAT GATGAGCATC ACTGGAAAGC TCACTGTGTG
33451 CCAGGGACCG TGCTGTGTGC TTTGCCTGTG TTCTCTCATG ATCCTTATAT
33501 TAATATAACC CACCAGGTTG ACACTATTTT CCCCATCTTA TAGGTGAGGA
33551 AACTGAGGCT TAGGTCAAGT AATTTGCCCA AAATAGTATT CAGAGGCTTG
33601 TACTGTGTTA CCTTTAGAGT GCTGATGGAA AGATGCTTTG AGTGCTGGCA
33651 CGGTGGATCT GGTGGGGAAC AATCTTACAG CTCTATATCT AGCCTCTACT
33701 CTGTGGTAAG ACCCCGTCTC TGTCATAAAA GTGCTCACTG GCTCTATAGA
33751 GGAGGTTATT ATACCCATGA ATAAAAACTA GGTTGTAAGT AACCATCAGA
33801 TGAGTTATGG GGCCAGTAAG TGCTGTAGAC ATTGCATTAT TAGAGCGATC
33851 CCTTTGTGAG AGGTAGTCAG AAAAAGTTTC TTAGAATTGT TGGGATTTAC
33901 GTAGCAGGAA GAGGAGTATT AAGGGCAGGA AGGCACCATA TTTTTAAGAA
33951 AGGTAAAAAT TTTTAAGGGG CGTAATAGTA TCTTGATTGT GGTTGAAGCA
34001 AGAAAGTAAT GGCAGCAAGT TGGGAAGATG AATGGGAGCT GGATTGTGAA
34051 AAGCCTCGAA CTCCAGACAA AGGAATTTGA ACCTTATTCT GTAGGCTCTG
34101 GGAAGCAATG GAAAGTGTAA GAGGAATTGC TTATATACAG TGTGAGTAGA
34151 ATCTAGGATT CCAATTTTTT TAGAAAGGGT GCCTACCTAG AATATTATTT
34201 TCTCTCTGTG ACTTCAGGTG TAGAATTGTC AGTACTTGTT TTTGAAGTTT
34251 ACTCATCAAA AAAGGAAAGG CAAATAAATA ACTGCAGCAA AAAATGACCC
34301 ATTAGAGCCT TTGAGATTCT TTAAAAAAAT TCCCTTCCCT ACCACTCTTA
34351 AAAATCAGAG TAATGGCAAA TCTGTAAGTT CTCTAGAAAA ATAATTGGAA
34401 AGAATTTATA AATTCTGAGT CTCGTCTTTC CTGTATCTGA TTCTGAAATC
34451 TTGAATGTGC TAATTCCTTA TATTAACAGG ACAATGTTTA TTGCCTTTGC
34501 TTCCCTGTGC CTTAGTCACC TTTCCCGGAT GAAAGGCATT CCCATGATAT
34551 TTTTAAGGCT TGCTTGCCTT TTCAAAGTTC ACTCTGTTTA TTCTGTCCTA
34601 CTTTATACCA GTCATGTGGC AGAAATCAGG CCTGCTCTGT GAATCGGCTT
34651 TGTGCAGATC ATGAGGTAAC TGTGGCTGTT CCACTTGTCA TTGATCATTT
34701 TCTTCTCGGC AGTCAGGCTT TTATGCCTTT TCAGAGACAG CATTTGCTTT
34751 GCACAACATA GACAGCAGGG TTATAATTAA AATTAGTAAA TTGCTGCTTT
34801 AAGTTTTGCT GGCTTTGTAA AAAAGACACC TTTTTTGGTT TGATAAACTT
34851 ATGTGTTTTT ATTTCATGCC ACACTCTACA TCTGTCATAA TTATGTGGGT
34901 GATTCTTGTC CAAATACAAT AAAGCAGGCT CTCACATTTT AACGTTCAAC
34951 AAAATACCTG GCTGGCTGAA CGTGGTTATT GCCAATTAGT GCATATGGGA
35001 TGAATACAGT TTTGTTCAAA AGGACAGAAT AATGGAATTC TGATATAAAT
35051 ACTGTTGACC CCAGATCCTT ATACTATAAT TAATAGATTA TTTCCTCTGA
35101 AAATAAAAGA GATTGGAGTT TTTCTTTTTT GTTGTTGTTT TTGGTCTGCA
35151 TTCTGAGTGG CTGTTTGAAC TGATTTTAAT TTCCTTCATG AAGATGATGA

FIGURE 3A-11

35201 TGTTTTAGCT GGCCCAGGGG CAGCCATTTC AGTGTGCATA AAGGTGGTTG
35251 CGTTGGGTAG GGGGATGCTC AGAAAAATCA TGGAAAGCAT GGGAATTCAT
35301 AGGGTACTTT GGACATTTTG GAATCTTGAA GAGTAAGAAC CGTAACTGGT
35351 GACTTAAGTG TCGTGTTTCT TCATTTCACC AAATGGCAAA ATGTGATACA
35401 GTTCTTCCAA TATCATGGGC AACTTGTAGC CAGAATTAAG TAGAAGATAA
35451 GATTAGAATT GAATATAATA ACTTTTGATT TATCATAGTG CCTTTTAAAT
35501 ACATAGTACC TCTTTGCTAT ATTATAGTGA TAGCTAAATG ATCTTTTCAC
35551 ATTCCTAAGT TTTGATTTCT GAATGGCGTC GCTCCTGCCT CCTGACATCT
35601 CACACTGTGA ATGTGCTACT TGCTTTCTCT AGGCGCACCT ATGTTGGCAG
35651 CATGCCTGGT CGCATCATCA ACGGCTTGAA GACTGTGGGA GTGAACAACC
35701 CAGTGTTCCT ATTAGATGAG GTTGACAAAC TGGGAAAAAG TCTACAGGGT
35751 GATCCAGCAG CAGCTCTGCT TGAGGTAAGA TTTGGAAAAT TCCCTGTCTG
35801 TCTTCATACT GGAAGAGTAT GGAGGAGGGT TGATAATCAT ATTCAAGTGA
35851 TATACACAGT GGTGTAGCTT TAGTTATGGG AAAAACAGTT TGATACCGGC
35901 TGAGGTCTGA GCAATTTGGC ACTTAAATTA AAATGTTTTT GAGATTTCTT
35951 TCACTAAGTC CCCTTTTTTT TTATTTTCCT TTTGTATTTT AATCAGATAG
36001 TTTAACAAAG TTTTGTGCAC ACTTATTATC TAGAGGCCAA CAATTCTACA
36051 CAGTTATGGC AAAAAAAACA GCAAGCAAGT CTCCTTCTCC CTGGGGTCCC
36101 CCATGCCTTC TTCTGCACTT TGACCTCTTC AGCTTTTAGT TGATTAACCC
36151 TATTTTCAAA ATAGCATGGC TATCTTGCAC TTCCTGATTT TTTTTTTTTT
36201 TAGTTTTTGT CATTTTCTAT AGATGCCCCC CAACAGGAGG TGAAGATTTT
36251 ACCTTTTTTC TTCCGTTGTC CCCACTGTAT CATTTTTATA CCTTAGATCT
36301 CGCAATAAGA ATTTTTTTCT TGTTTTTTTG TTGTTTTTTT CTTGTGAATA
36351 CTAATACATC CATATTAGTA TTTACATTAT TATGATTATG TAAATGCTTT
36401 TCACAGCAGG AGCCACATGG TAAACTGTGA TCACTTTTCC TGTTCCTATT
36451 TTTGTTTTTC TCTACTTTTT AAGAATATTT TCAGAGTTAG CTGTCTTGTT
36501 TCTTTTGTTT ACTTTTTCAC CAATCGTCTA ATTCTGTCAA GACCTTCAGA
36551 CACTTTAGGT GTTCTATCCA TTTTATCTTC TTAAGCGTCC GGTCTGAACT
36601 GGTTGTTTTT GACATCCGGT TTTATGGCTT CCTTCCTAGG TTCTCCCTTC
36651 ACCTCTCACC ATGTTGGATT TCCTGTCTCC TGTATTCCAT TTCTTGCTCT
36701 TTCTTGGTCC ATTCCCTCAT TTTTGTGGTG TTAACTCCCT GATAGTTTCC
36751 TGAGAAAGCT TGCATGAGTG GTAAATGTTT TAGACTTTGC ATATCTGAAA
36801 ATGTCTTTAT GTTTCCCTCA TACTTGATTA GTAATTTGAG TAAAGAATTC
36851 TGGTTGGAAA TAATTTTTCT ATAGAATTGT ACTTTGCCTC CATTTTACTT
36901 CACTTTCCCA TTTCCAGTGT TGCTGTTGGT AAAACTGATT CCATTCAGTT
36951 CCTATCCTTG CAGACCTGCT TTACCCTGAA AACTTTCAGG TTCTTCCCTT
37001 TATCCTGGGA TTCTGAAATT TCCTAATAAT CTGCCTTGGC ATGGGTTTCT
37051 TTTCATGCAT TTTTGCTCAT TCTTTCTTTG AATTCTTCCT GTTCTTTGGT
37101 TCTAAAATTT TTCTTAAATT CTTTTATTGA TGACTTTTCC CCTTTATTTT
37151 TTGGAACTCC CATGACTTGG ATATTATGTT TCAGACTTAT CTTTCTCTC
37201 CTATTAGTCT CCACTTTTAT GTTTTGCTCT ACTTTCTGTG CAGACTTTCT
37251 CAGATTTATC TTTTAAAAAC CCTCTGAATT TATTATTTCA AAAACTTTCT
37301 CTGCATGTTC TTTTATAGTA TCCTGTTCTT GTTACATAGT TGTAATATAT
37351 CTTATCTCCA TGAGAAAGAT ACTTATAGAT ATATTTTAAA ATTTTACTTC
37401 TCTGACCACT TGGTATATTA AAAAGAAAAA GAAAAAAATT ACTTCTCTTT
37451 AAGCTGCTTT TATCTGTTTA TTATATATTT CTTTTAGTCT CTTTTATATT
37501 AGAGTCTTTC ATTAGATATC TGGACATTTT TGTTTGTGTG TTTATATTTA
37551 ATAGTAAGGG ACAAAAAGGC TGATTGGAGG CTATGAGCAT AGGAGTGGGG
37601 CTTATCAACA GTGAGTTCCA CAATAGAGTC AGCTGGCTGT GCTGTTTGGT
37651 TGAGGAATCT TCTACTCAAT AGCTTTAAGT CTTCCTTCTT AGGATGGTCA
37701 GATTCCTCAG AGAAGACTTC CTGTCTCTTG CCTTGAGAAT GAAGGCCTGG
37751 CTGCCATCAT TCTGGGAACC AAGCAGGGGA AGAATGATTG GGGTCGGGGG
37801 TATCACTGCA TTCAGCATCC GTGTATATGC ATTCACCTGA GCTCTTGTTT
37851 TCAGCATAGT ATATGTTCTT ATCAGCTGTG CCCAGGGTCC CCTGTGCAGA
37901 GAACCACTGT TTTATGTTCT TAAGAAAATA AACTTCCAGT GTTTTGCTGG
37951 GGTGGGGGAG GGGATCTGGG ATCTGACTGC TTCCTAAATT TATTTCAGCC
38001 AGTCCTCCTT ATTTTAGCAC ATCAGCCCCT CCTCCCTTTT ACCCTTGCTT
38051 AAAATATTAT TAATGCAAAT TGATTTGTAA AATTGAGGAA AACTTACTTT
38101 GTGAAAGTTT TTATTTTTTT CTTGTTTTATT TCTGTGCTTT GAGCTGCCTC
38151 GTGCTTCCTG TTTTTTTTCT GTTTTTGTGA TCTTAGAACA GGATGGCCTG
38201 GGACATGTGT CTTATTAAGC AGGAGACCAT ACATTCTGGT TTGCTTGGCA
38251 CATTCCCAGT TTATGCCTAA TATTAATTGC ACTCTTTTTT AGTCTCAGAA
38301 GTGGGTTTTG TTTGGACGAT AAAAAAGTAC AGTTACCTTA CTTAAAAGCC
38351 CTGGTATTTG GAGGTAAGGG TTTGATTTGG TTCAGTTTTG CTACTTTTTA

FIGURE 3A-12

38401 TTGTAAGATC ATTACCTTCT GGCTCCATAA CTGGTTCTTT TTACTATGAA
38451 GAGTAAAATA GTGAACATTA TTTAAGATTT TAGTAGTTTC TTATATAATA
38501 TCTTTAGACT TTCAGTTTAA TTTATATTGG GACATTTTTT CAGGTTATCT
38551 GACAGATTCT CCCATTAGAC ACTTACAGTT ATCCTGTTGA AAATAATTTT
38601 AGAGTATTCC CCTGACACTT AAATTTTTTC AACAACTGTT TTGAAGCAAG
38651 TTCACCAAAG ACAGCTTTAC AAGTAGTAGT AGATGATTAA GTCCCCTGTT
38701 TATTTGTTCA GTTGATAAAC AATATGTTTT AGGTCTTCAC CTATATATAC
38751 TTTGTAATGA TTCAATAATA TTTGTTAAAT TGATCTTTGA TAACAAGCAG
38801 CTAGCATAAT GATATTTTCT TGTCTGATGT AGACCTTGGT ACTCACTTTT
38851 TTGGCAGTCG ATTTATTAGC ATTCAAAAAA AAGGTATGAA AACCTCAAAT
38901 GATATCTCAG AGTAAATGCC CCCTGGGCCC ACGTACTAAT CACTGTAGTT
38951 TAGTTATGAA TAGCATTGGT TCCTTACAGA CTGTAAATGC TATAAAATGA
39001 AGCAAGACAT ACATATGGAG GAACTGAGTA TCTTGGTAGC TGACAGCCTC
39051 TTCCTCCCTG CTTGCCCAAG TCCTGGGTAA AAACCTCAGA CCTCACAGAT
39101 TGTTGAAACA ATTAAATAAC AGTACATATT AAAGCACTCT ATAAATGGTA
39151 AAGTACTGTA CAGATGTTAA TTTAATATCC ACTGATATTT CTTCTGTGTC
39201 CATTTTGAAA GCCACTTGCT GCTTCCATTG CCAGTAGGTT CACTTAAATT
39251 TAAAAAAAGA ACAAACTCAA TTACACAACA CGTTACATTT AAAGTGAATA
39301 TTCCTGAGAG TTTGGAGACC CAAGTATAGT TTTATTATCT TTCTACATAG
39351 AAAACCTGCT TTTAAAAAAT GATATCTAGA TATTATTTGT AAAATGTATA
39401 AGATTATTTT ATGTTTAAGC TAATTATATT ATTAAGGTAA TATAGCCCAG
39451 ATGTGAAGAA TGTAATAGTA GATGTAAATA TACACTAGAG TGCTTACTCT
39501 GAATAAAGAA TAAACTTTTT CTGCTGTGTA TTCTTCTTTT TATTTATGTA
39551 GGATATGCCC GTTTCCTTGA CCTACCATGT AATTGTTGCT TATGTAAAAC
39601 AGAATGTATT TCAAGTTATT ACTTAATATT GTCCAAAAAA GGAGAATTCA
39651 AAATTTAGAT GATCTCTTTT GAAAATTTAT TGGAAGACTA TAAAAATAGG
39701 TCCAACTACT TAATTAATAA ATGGTGGTAG GCAGTAGAAT TTGGGCAAGT
39751 CTATAACTGA GTAGCACTAA AATATTAGAT ATAAGGAAAG TAAGGGCTTG
39801 TATGTAATTA ATAGACTTGA AAGAAAATTA CAGAATTATT TTCTTACCAG
39851 ATATATGTTA TATTTATAAC TGGCACATGT CCAGACTTTA TTGTTAAATA
39901 TGAATGCATA TCTCAAATAC ATTTTTGTGT GAGTGGGCAA ATAAAATGCA
39951 TGGATACAAT AATTAATTGT CTTTATAGGC AATAATATTT ACAGTTCGAA
40001 AAACATATAT TCCCCAAAAT AGAGAAGTCA CTAGTCTAGA TATAGTAAAC
40051 TTCCTTTAAA ACTGAAGTTC TTACTTAATT CGAATTAGAT CCAGTTAGTA
40101 ATTAGACCAA TAGTATATTT ACTACTTAGA TACAGTAGAC ATGATCTTTT
40151 GATTTGAGCT ATACAATTAT TGTCAAAGAA TGTCAGAAGA GAGGGACTTA
40201 GACATCATCT AATCCAGCTT CATGCTCTTA AGGATAAAAA GCTTAAGGCC
40251 TAAGATATTA TTTTAATTTC TTATTTCACT ACATGCTATA TTAATGATAT
40301 AATTTCCAAA TATCGAATGG AGTTAAAAAA TGCCTTAAAT AAGGCATACC
40351 TTGTTTTATT GTGTTGTGCT TCATTGTACT TCACAGACTG TGTTTTTTTA
40401 ACAAATTAAA TGTTTATGGN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNGGGCAC CCGTGTATCC
40501 CCAGCCCCTC GGAAGCTTGA GCCAATAACA ATACCTTGAC CCGGGGAGGC
40551 AGAGTTTGCG GTCACCGGAG GGGGGGGGGG GGCGTCGCAA CCTGGGTTAC
40601 AAACCAATAC TCTTTCTCCC GTCCCCGACA AAAAAAAGAA AGAAAGTGTT
40651 TATGGCAACC CCGTGTCAAG CAAGTCTGTT GACACCATTT TTCCAACATC
40701 TTACTTCATG TCTGTATGTC ACATTTTGGT AGTTATTGCA ATATTTTTAA
40751 CTTTTTCATT ATTATATCCT ATTATGATGA TCTGTTATCA GTGATCTTTG
40801 GTATTGCTAT TGTGATTGTT TTGGGGCACC ACAAACTGCA CCCATATAAG
40851 ACAGCAAACT TAATCAATAA ATGTTGAGTA TGTACTAACT GCTCAACTGG
40901 CCAGGCATTC CCCTTTCTCT CTCCCTCTCC TCTGGCTCCT ATTCCCTGAG
40951 ACACAGCAAT ATTGAAATTA GGCCAAGTAA TAACCCTGCA GTGGCTTCTA
41001 AGTGTTGAAG TGAAAGGAAG AGTCACACAT CTCATTGTAA ATCGAAAGCT
41051 AAAAATAATT AAGCTTAGTG AGGAAGGCAT GTTGAAAGCT AGGCCTCTTG
41101 TGCCAGATAG CCAAGTTGTG AGTTCAGAGG AAAAATTCTC AAAGGAAATT
41151 AGAAATGCTA TTCCAGTGAA CACACCAATG ATAAGAAAGT GAAATGGCCT
41201 TATTGCTGAT ATGAAGAAAG TTTTAGTGGT CTGGATAAAA GATTAAGCCA
41251 ACTACAACAT TCCCTTAAGC CGAAACCTAG TCCAGAGCAA GGCCCTAAGG
41301 CTCTTCAGTT CTATGAAAGC TGAGAGAGGT GAGAAAGCTG CAGAAGAAAA
41351 ATTTGAAGCT AACAGAAGTT GGTTCATGAG ATTTAAGGCA AGAAGCCATT
41401 TCTACAACAT AAAGTGCAAA GGGAAGCAGC AAGTACTGAT GTATTGTAGA
41451 AGCTGCATCA TGTTATCTAT CCAGAACATC TAGCTAACAT CATTGATAAA
41501 GGTGGCTACA CTAAAAAACA GATTTTCTAT GTAGATGAAA CAGCCTTATT
41551 TTGTATTGGA AGAAGTGTCA TTTAGGACTT TCATGGCTAG AGAAGTCAGT

FIGURE 3A-13

41601 ACCTGGCTTC AAAGCTTCAA AGGGCAGGCT AACTCTTGTT AGGGGCTAAT
41651 GCAGCTGGTG ACTTTAAGAT GAAGCCAGTG CTCATTGACC ATTCTGAAAA
41701 CCCTAAGGCC CTTAAGAATG ATGCAAAATC TACTCTGCCT TTGTTCTGTA
41751 AATGGAACAA CAAAGCCTAG GTGACAATGC ATCTGTTTAT AGCATGGTTT
41801 TACTAAGTAC TTTAAGCCCA CTGTTGAAAC TTACCGTTCA AAAAAAATAG
41851 ATTCTTTTGA AAATATTACT GCTCGTTGTC AATGCTTCTG GTCACCCAAG
41901 AGCTGTGATG GAGATGTACA AGGAGATTAA TACTGTTTTC ATTCCTTATA
41951 AAACAACATC CATTCTGCAG CCCATGGATC AAGGAGTTAT TTTAACTTTC
42001 AAGTCTTATT ATTTAAGAAA CACATTTTTT AAGGCTATTG CTCCCATAGA
42051 TTATGATTCG TCCCATGCAT CAGGGCGAAG TACATTGAAA ACCCCTAGAA
42101 AAGATTCACC ATTCTAGATG CCATTAAGAA CATTCATGAT TCACGGGAGG
42151 AGGTCAAAAT ATCAACATGA ACAGGAGTTC AGGAAGAGTT GATTCCAGCC
42201 CTCATGGATG ACTTTGAGGG GTTCAGACTT CAGTGGAGGA AGTTACCGCA
42251 GTTGTGGTAG AAATAGCAAG AGAACTAGAA TTAGAACCCA AAGATGTGAC
42301 TGAAATACTG CAATCTCATG GTAAAACTTG AACAGATGAG GAGTTGCTTC
42351 TTACAGATGA GCAAAGAAAG CGGGTTTCTT GAAATGGAAT CTAGTCCTGG
42401 TGAGGATGCT ATGAACCTTG TTGAAATGAC AACCTTGATG TTGTGAACCT
42451 TGTTGAAATT CTAAACAAGA TTTAGAATAT TACATAAACA TAGTTGATAA
42501 AGGCAGCAAC AGGGTTTGAA AGGATTGACT TCAATTTTGA AAGAAATTCT
42551 ACGGTGGGCA AAATGCTATC GAATAGCAAT GCAGGCTATA AGAAATTGTT
42601 TCATGAAAGG AAGAGTCAAT AGATGAAGCA AATTTTACTG TTGCCTTATT
42651 TTAAGAAATC GCCACAGCCA CCCTAACTTT CAGCAGCCAC CACCTGATCA
42701 GTCATCAACC ATTAATATTG AGACAAGACA CTCCACCAGC AAAATGACAA
42751 CAACTAACAC TGAAGACTCA GGTGATTAGC ATTTTATAGC AAGAAAGTAT
42801 TTGTTAATTA AGGCATGTAC ATTGTTTTTT AGACATAATG CTATTGCACA
42851 CTTAATAGAC TATAGTATAT TGTGTAAACA TAACTTTTAT ATGCACTGGG
42901 AAACAAAAAA AAACATACAT GTGACTCACT CTGTTGCAAA ATTTGCTTTA
42951 TTGCAGTGGT CTGGAACTGA ACCCACAGTG TCTCTGAGGT ATACCTGTAT
43001 TGAGGAGGGG TTGCAAATTT TAGCACATAG GCAAATTTGC AAATATGGAA
43051 TAATAAGGAT CAACTGTAAT TACTGCTTTA TGCCATTATC TTTTAAATCA
43101 GATAAGAAAA AGTTACGTCA ACAATATATT TACACTGCCT TTTATGTTTG
43151 CAATGTAATC ACTTCTGCCA GTGCGCTCTA TTTCTTTGTG TGGATACTGT
43201 CTAGTGTCCT TAAACTTCAG TCTTTCATAT TTCTTGTCTC ATCTCCTGGT
43251 GACATATTCT CAGTTTTTGT TTTTCTGGGA ATGTCTTAAT TTCTCCTTCA
43301 TTTTTGAAGT AATTTTGTTG GTATAGAATT TGGGTTGACA ATTGTTTGCT
43351 TTCAGCCCTT TCGCATGTCC TCTCACCACT TTCTGGTCTC TGTGGTTTCT
43401 GCTGTGAAGC CAGCTGTTAA GCTTGTGGCG GATCTCTTAT GCCTAATGAG
43451 GGCAGCATTT TTCTCTCATA GTTTTCAGTA TTCTCTCTTT GTCTTTCATT
43501 TCTGACAGAT TGACTGTGTT TATGTGTGAT CCTCTGAGTT TACTTAGTTC
43551 TTTTTGAGCT TCTTGGATGT GTAGGTAAAT GTTTTTCATC AAATTTGAGA
43601 AGTATGTGGC CAGTATTTCT TCAAATATTC TTTATGCCCC TTTCTTTTTC
43651 CTCTCCTTCT GAAACTCGTA TTATGGTGTG TTGGTAATCT TTGTGGAGTC
43701 CCGTAGGTCT CTAAAGTGCT GTTCACTTTT TTTAAAGCCT TTTTTCTTTC
43751 TATTCTTCAG ACAGGATCAT CTCAGTTGAC CTGTCTTCAA GTTCATTGAT
43801 TCTTTCTTCT GCCAGCTGAA ATTGTCATTC AGCCCCTCTA GTGAATTTTT
43851 CATTCAAATT ACTGTAGTTT TCAACTCCAA AATTTCTATT TTAAAATTTT
43901 TATTATTTAT CTTTGTTTAT ATTCTCTATT TGTCAAGACA TCATTCTCAT
43951 ACTTTCCTGT AATTGTTTAG ACATGATTTC CTTTAGTTTT TTTAAATGTT
44001 AGTAAATATA ACAGAAAAAG TCCCATTTTT ACCACTTTTA TGTGTACAGT
44051 TCAGTAATGT TAAGCACATT CGCATTGTTG TGCAGCCAAT CTCCAGAACT
44101 TTTTCATCTT GTTAAAGTGA AGGTGTATAC TCATTACACA GCAATTCCCT
44151 GTTTCTTTCT CCCTCCCTCA GTCCCTGGCA GCTACCATTC TCTTTTCTGT
44201 TTCTATGAGT GACTACTCTA TATACCTCAT ATAAGTGCAT CATACGGTAC
44251 TTATCTTTTT ATAATTGACT GACTTCACTT AGTTTCCTCA AAGTTCATCA
44301 ATGTTGGGGC ATTAGTTTTT TAAGCATATT TATAGTAGCT GATTTGTAAT
44351 CTTTTTTTTT TTTTTTTTGA GACGGAGTCT CACCATGTTG CCCAGGCTGG
44401 AGTGCAGTGG CGGGATCTTG GCTCACTGCA AGCTCCGCCT CCCAGGTTCA
44451 CACCATTCTC CCGCCTCAGC CTCCCAAGTA GCTGGGACTA CAGGTGCCTG
44501 CCACCAGGTC TGGCTAATTT TTTGTATTTT TAGTAGAGAT GGGGTTTCAC
44551 CATGTTAGCC AGGATGGTCT CGATCTCCTG ACCTTGTGAT CTGCCCGCCT
44601 TGGCCTCCCA AAGTGCTGAG ATTACAGTCG TGAGCCACCG TGCCTGGCCG
44651 CTGATTTGTA ATCTTTATCT AATAAATCCA ACATGTCTTC CTTAGGGATG
44701 GTTTCCATTG ACTTCTCTTT TTCTTTTTTG AGACAGGGTC TCGCTCTGTC
44751 ACCCAGACTG GAGTGCAGTG GCGCACTCAT GGCTCATGGC AGCCTTGACC

FIGURE 3A-14

44801 TTACCCAGGC TCAAGTGACC CACCCACCTC AGCCTCCCGA GTAGCTGGGA
44851 CTACAGGCAC ACACCAGCAT GCCTGGCCAA TTTTTTGTAG AGACAGGGTT
44901 TCGCCATGTT GCCCAGGCTG GTCTCGAACT CCTGAGCTCA AGCAATTTGC
44951 TCACCTTGGC CTCCCAGAGT ACTGGGATTA CAGGCATGAG CCACTGAACC
45001 CAGCTGACTT CTCTTTTTTT TTTTTACTCT TTAGGGCCGT ACTTTTGTAT
45051 TTCTTTGTGT GTGTCTCATA ATTTTTTTTG TTGAAACTGA ATATTTAGAG
45101 TGTTATATTT ATATTAAATA CAGTCAGATA TATAATTGAA TAATATAACC
45151 TTAAGGGTTT TTTGTTTGTG CTGTTGTTGT TGCTGTTTGT TTAGTGACTT
45201 TCTGGTTTCA TTCTGTAAAG TCTGTTTTAT TCATTAATGT GTGACCACTG
45251 AAGTTGCTCA GTTTGTTTAG TGGTCAGCTA GTGACCGGAC AGAGATTTCC
45301 TTAAGTACCT GGACAGTAGC TCTCCCACTC CTTGCCCAAG GGGCTCTTAT
45351 GTGTGTATTG AAGTGGGCCT TTCACACTTT GGCAGATGGT TTACAACTCT
45401 GCCTTAGCCT TCACTTCCTG CTTTTGCAGA GCCTCAGTGT CTGCCAAAGA
45451 TGAGCTTATA GGGCCTTCTC AGGTCTTTCC TGGATATACT TAGAGCCTGC
45501 ACATTCACAT GAAATTTTGG ATTCTCAGGC ATATGTCAAG GCTTTTCAAA
45551 GTCCCCATGA ATATCTCATT TCCCAGTTTT TCCATTTAAG TTTTTTGGTC
45601 AGCCTCTTGT TAGTCCCAAC TAGTTTCATT GCCTCAGGCA GCTGCAGTGC
45651 TAAAACAGTT GCCACTGGTT GTTTTTGGCA AATGTCCTAA GGATAAAACT
45701 GTTCTCACAG AGTGTTCTCT GAGTTAAGTC AAATAAGGAT ATGGAGCTCT
45751 TCTAAGGAAC TGCCAGAGTC AAACAGGGAC AGTTCTCTGG GGATGGGGCT
45801 TTTGAAGGAT TGTAATCCTT TTCTACCCCC TAACAGGATT GCTAGGCTAC
45851 TGGTTTTCAC AGCTACTGGG GTTATGAGGC TGTTGATTTT GCTACCATGA
45901 ACTTGAGAGA AAGGGATGAG TGTAAAGCAA GTTAAAATAT CACAAAGCTC
45951 GTTCTGTTTA TTGAGATTCA GCTGTTTTTC TTGAATAAGC ACTCCTCAAA
46001 TTGTTGCAAG TTAGTATGTA GCATTCTGAA AAAGTTGATT TTGACAATTT
46051 TTGCTAGTGC TCTCATTGCT TTTCTGGAGG AGCAGATTTT CAGAGTTTCT
46101 TACTCTACCA TTATATAATA GAAGTGCTTC CTCCCCCATT TCATTTTGAT
46151 TCTGTGCTTG AATGATTTCA CTGCATGCTT CTGATACTTG TATTTTGGTT
46201 TATCACTTGT TCAGATGAAA TATATCTTCA GGTTACTTCA TTCAAAGATT
46251 TGTGTGTGAG TTGTATTTTG AATCTCTTCT ATATTTGAGA AGGCTTCTTT
46301 GTTGTCTGCA CCAGTAGTAA TATATATGTA AATAAAATAA GAATGTATTA
46351 GTCTTCTTCT TTTTTTTTTT TTTTTTTTTT GAGACGGAGT CTTGCCCTGT
46401 CACCCAGGCT GGAGTGCAAT AGTGCAATCT TGGCTCACTG CAACCTCTGC
46451 CTCCCAGGTT CAAGCGATTC TCCTGCCTCA GTCTCCTGAG TAGCTGAGAT
46501 TACAGGCACG TGCCACCACG CCTGACTAAT TTTTTGTATC TTTAGTAGAG
46551 ATGGGCTTTC ACCATGTTGG TTAGGCTGGT CTCGAACTCC TGACCTCGTG
46601 ATCCATCCGC CTCGGCCTCC CAAAGTGCTG GTATTACAGG CATGAGCCAC
46651 CGCGCCCAGT CAGAATGTAT TAGAATGTAT TTCTTAAGAC TGCCATAACA
46701 AAATACCACA GACTGGGTAG CTTTGAAGAC CAAACAGAAA TTTATTTCCT
46751 TATGGTTTTG GAGGCTAGAA TTCCAAGACC AAGGTGTTTA TAGGTTTGAT
46801 TTCTCCTAAG GCCTCTCTCC TTGGCTTACA GACAACCGAC TTGTGGCTGT
46851 GTCCTCGGGA GACCTGTGTG CATGCATCCC TGGGGTCTCC TCTTTCCTCT
46901 TATAAGGGTA CCAATTGTAT TAGACTAGGG GCCCACTCTT ACCTTCATTT
46951 AACCTTAATT ACCTTCTTAA ACACCCTGTC TCCAAATACA GTCTTCACCC
47001 TGACTGCCCT TGAGACAGAG CGGAGGGGGT TAGGGATTCT GTCAATTTTG
47051 AGGGGGCACA ATTCAGTCCA TAACAAAGGA CATATATAAT AGATACATAA
47101 TATATATGTA CCAGTGTGCC CATATCATGT ACTTTATGTA AAACGAAATC
47151 AGTTTTAAAA GGTAATTATA TTTTCAATGA AAGCACTGTG TTCTAATTAG
47201 ATAATTGTTT TTACTTCATA ATATGTCTAT CCTAGCTTAT TATATAAATA
47251 AAAGTGTCAA CTCTGTTATT TTCTTGTGGT TCATACCTTT GCCTATACCC
47301 TTTTTAATGA TACTTTGCAG GAATCTTTTT AAACCACTCA ACCCATTTGT
47351 AATATTAGGC TCTGTGAACC CGGAAAATTT GAGACAGGTC TCAGTTAATT
47401 TAGGAAGTAT ATTTGGCCAA GGTTGAGGAC GCGCGCCCAT GACACAGCCT
47451 CAGGAGGTCC TGACGACACG TGCCCAAGGT GGTCAGAGCA CAGCTTGATT
47501 TTATACATTT TAGGGAAGCA TGAGACGTCA ATCAGCATAT GTAAGGTGAA
47551 CATTGGTTTG GTCTGGAAAG GCAGGACAGC TCTCTGGAGA GGGCTTCCAG
47601 GTCACAGGTA GATAAGAGAC AAACCCTTGT GTTCTTTTGA GTTTCTGATT
47651 AGCCTTTCCA AAGGGGGCAA TCAGGTTTAC CTCAGTGAGC AGAGGGGTGA
47701 CTTTGAATAG AATGGGAGGC AGGTTTGCCC TAAGCGTTCC CAGCTTGATT
47751 TTTCCCTCTA GTCTGGTGAT TTTGGGGGCC AAATATATTT TCTTTTCACA
47801 GCACACATGG ACAGCAATGT GCTGTAATTA TAGTTAAGGC AGATAAGTGA
47851 GGACACCACA GGCAGCCTTC GACCTTATGG AACTTCTTCT AAGTGAAGAC
47901 ATCAATTCCA TTTTGGATAT TAAATATTTA CAAGCTATTT TTTTCTGGTA
47951 TTTATAAATA AAAAAGATAA ATACAAATAC TAATATTTTC TACTTGCACT

FIGURE 3A-15

48001 TTGGTGGGTC ATTTTCCACT TTTGTGACCA CTGGTCTAAA TAGATAAACA
48051 AATGTCTTCA CAAATGGGTA GTAGGTTCAC AGGTGTTCAT TTTGTTATTA
48101 TGCATCATAT CTTATATATA TTACATATAT TTGATGTATT CAAGATTGTA
48151 AAATATTTTA AACTAGTGAT AATTTTGCTT GAAAATTCTG TAGGTGTTAT
48201 TCTAATGACA TTCTCATTTT TATTGCACAG GAGGAGGAAT CTAAATCTTT
48251 TCAATCTATA GTGTCAAGGT CTTCTAGAAT ATTTTCGTTT CTTTAATCCC
48301 TATTTTAATT TACTGAGACC TCTTCTTTAG TTATATTAAC CAGTTATGAA
48351 TTGTATCTCT TAATTTTTCC CGTATTTATC CCCTACATGT CTCTAAAGCC
48401 CTTTTTCTTC TATGTCCTGA ACACTTTTCT CAAGTTTGTC TTTATCACAG
48451 ATTTAATTTC CATAGTTGAG GATATAGAGG AAAAGTAAAC TCAGTTTCTC
48501 CTACTGCACT CTCACAACAC AGAACACCTC TGACCAAATG CACGGGTTTT
48551 TTCTCCATAT GCCAAGCAAG CAGTTCTTCA GCAACCGACC ACAGCTGGGT
48601 GTCCTCTAAT TCAATTCTGA CAAAGTGTAT CAGATCCTAC GGGTTGAGCA
48651 CTGAGTCCCA CAAGACTGCC TCCCCCTTCA GATGCCAGTC GTGAGTTGAC
48701 TTCCAGAACG TGTGACCAAC CAGTTATAAA TTGGAGTACC CACAAGCCCC
48751 CCTCCTCAGG TTTGCTTAAT TTGCTAGAGT AGCTCACAGA ACTCAGGGAA
48801 ACAATTTACT TGCATTTACT GGTTTATTAA AAGAATATTT TAAAGAATAC
48851 AAACAAACAG CACAGGAGCT TCCATCCCAG TGAAGTCAGG GTCCACCAGT
48901 CTTCTTGCAC CTGGGTGTGC TCAAATTCAC CTTCCTGGAA GCTTCCTGAC
48951 CTCAGTCCTT TCGGGTTTTT AATGGAGGCC TTGTCACATA GGCCTGATTG
49001 ATTAAAATCAC TGGCCATTGG TGATCAACTC AACTCTTAGC TCTTCTCCCC
49051 TCCCAAGAGA TTGGGCTGGG GAACTGACAA GTCCTCAGCC CTCTAATCAT
49101 GCCTTGGTCT TTCCTGTGAC CAGCCCACAT CCTGAAGCTG TGGAGGGACT
49151 GCCAGCCACC AGTCAATCAC TAACATACAA AATGATACTT ATCACTTTGG
49201 TGATTCCAAG GATTTTAGGA GTTGCATGTC AGGAAACAAA GAGATGAAGG
49251 CCAAATATAT ATTTTACAGT ATCATAATAG TATTAATTGT GTGTGGCTTT
49301 CAGAGCTGAT TTTAGTTATG TTATTTTATC TTTATTTTCT GTTGTGGAAA
49351 ATTTCAACCA TAGCAAAAGC AGAGAAGATA GTATAATGAA TTCTGTGGAC
49401 TCATCACCCA GCTTTAATAT CTTGTTTCAT CTATTGCTTC CCATTCTCCC
49451 CTACCCAACC TCTGATTATT TTGAAGCAGA TTCCAGACAT CATCTTTTCA
49501 TAAATGTTTC AGTAGCTATC GACAAAAGAT ATACACTTTT AAAAAGCATA
49551 ATCATACTAT ATCACACCTA AAGATGACAG TTACCTAGTC TTGTGTAATG
49601 AACTCTATGT AATCTATTCC TGGATTGCCT ACAGACATCT ATAGTTCTTC
49651 TCTTGTCAGA AATTATTATT GAAGAATAAT TCTCAGTGTA CATTCCTCCC
49701 ACGGTTCATC CCATTGTGAC TTCACATTCC TAGGAATAAT GCGTCATATC
49751 ACAGCTATTT CCATTCCCAG TCATACTTTG TAGGTAGGAA TTATAGTCCT
49801 AGGATTGATA CAGAAAATCT TTTAGTTGGG GAGAATAAAG GAGAAACAGC
49851 CCTAATTATT TTTGAAAGTG GCCCTGGATG TGGGCAGTAG AATCCCTGCT
49901 CTGAAGTTAG GGTAAGAAGA TGAGGTTTGA TAGCTACAAA GCTCTTAATT
49951 GTAATTTTCG TCCTTCCATG GACTCACCAG TTTGCCTCGG AGCTTCATCT
50001 GAGTAGTGAT TACCAGAAAT TATTTTCTGC CAGAATATTG ATCAGTATTT
50051 CTGATGCTGT TTAAATTCTA TATGTCTTTT TATGCTTTTG AAAACCAGAA
50101 AGTATCTGAG ACAGGTCTCA ACCAGTTTAG AAGTTTATTT TGGCAACGTT
50151 CTCCAGAGAT GATTGTGAGG GCTTCAGTAT TTAAAGGGGA ATGGGCAGAT
50201 ATTGGGGAAA GAGGAAGAAA TTTTAAAAGG TATGAGTAGA CAAGAGACAA
50251 ACGGTTGCAT TCTTTTGAGT CTTTGATCAG CCATTCACCT GTGAGAGGGG
50301 AGCAGAGGAA TAGTCACTGA CGCATTCATC TAGCTTAGTG AATCTGCATT
50351 TCTACATAAG ATAAAATAAA TATAGCGTAC AGGAAGCCAT CAGATATGCA
50401 TTTGTCTCAG GTGAGCAGAG GGATGACTTT GAGTTCTGTC CTTTGTCCTG
50451 TATGTGTAAA GAATAAGCTA TCAATTTACA TGGTTGGGGT GAAATTCAAC
50501 AGAACTGTTA CAGGTTAAAG ATCTTGGGGC CTACAAGGAA TTTCTCAGTG
50551 GGGGGATTGT GAGGGAGATA TGTAGCTTTT TTTGTCTTTG TAGCTATCTT
50601 ATTTGGAAAC AAAATGGGAG GCAGGTTTGT GTGACGCAGT TCCCAGCTTG
50651 TCTCTTCCCT TTTGCTTAGT GATTTGGGGG TCCTGAGATT TACTTTCCTT
50701 TCACACTCTT CCTGAGTAAA AGAGGAAGGC AGGCAAATTG GGCACAAATT
50751 TAGCCTAAGT CTGCCTCCTT ACATATTAAT ATTTTAAGTT TGGCCTAAAG
50801 GTTTCCCCTT ACAAAGTAAA CTGCAGCCTA ACTAGCTGTG TAAACACACT
50851 ATTCTTAACA CCAATCACAG ATTTTCAGCA AGTCACAGGA AGTCAGCTGT
50901 TAACAAACTT TAAATAAAGC AAACACCAAG CTGTAAGCAA TCCCGCTGTT
50951 TCTGTACACT CTTTGTTTTC TGCATGTCGC TTTCCTTTTT CTGTCCATAA
51001 ATATTATCAA ACCATATGCC AGAGTTTCTC TGAACCTATT CTGTTTCTGG
51051 GAGCTGCCCA ATTTGAGACT TGTTCTTTGC TCAATTAAAC TGTTAATTTA
51101 TCTAGAGTTT TTCTTTTAAC AAGCATCACT AATTTTTTCT CCTTATAATC
51151 TAGGTATTCT GTCACACTGT TTTAAAAACC TCCTTCATAA TTCAGAAACA

FIGURE 3A-16

51201 TTGCTTTATT AATTTTCCTA CTTTTTAAAA ACGCTAGTGT CTTAAAATTT
51251 TAAGAGAAAA AAATTACTTG TTCAAGTCTG ACAGCCATTT CTAAAACATA
51301 TCCAGCATAT ATGAATTACA TATGCTTAGA GCCATTAAAG AATAGAATTT
51351 TTTCCGGCCA GGCATGGTGG CTCATGCCTG TAATCCCAGC ACTTTGGGAG
51401 GCCGAGGTGG GCAGATCACG AGGTCAGGAG ATCGAGACCA TCCTGGCTAA
51451 CATGGTGAAA CCCCATCTCT ACTAAAAATA CAAAAAAGTA GCCGTGCATG
51501 GTGGCGGGCG CCTGTAGTCC CAGCTACTCG GGAGGCTGAG GCAGGAGAAT
51551 GGCGTGAGCC CGGGAGGCGG AGCTTGCAGT GAGCCGAGAT CGCGCCACTG
51601 CACTCTAGCC TGGGCGAAAG AACGAGACTG TCTCAAAAAA AAAAAAGAAT
51651 AGATTTTTTT CCTTAGCTAG TGTTAAAAAA TTACTCATGA CGCTTATTAA
51701 AGGTGGTAAG GATTACTTTA TTCAAGGTGG GAGACTACGT ATAAGAAACA
51751 CTGCAATGGG GTTTTGCAGT GACAGGAGGA GAGTGAATGG GGAATCAGTA
51801 GAGGGAAACA TTCTAAGAGG AAGAATTGGG GTTACGGGGG ATTCTCACTA
51851 GAAGGACACA ACAGAACTCT TGCTGAAGGG AGGCCAGGGT GAAAAGATAC
51901 TGGGTTAGAA GTGAGAACAG ATACGTATGG GTATGGGTCA TTTTTGCTAA
51951 CCTGACTTAG CAGGATTCTT GCTCAAATTG GATTTTACAA AGACAGAGGG
52001 AAGGCTGACA TTGGCCTAGT TGAGCAGAGG ACTCAGAGGA GCCTGACTCA
52051 AGTTTGCGTC AAAAGAAGAG CGTTTTTGTC ACTAGATGAT AGTTTTAACT
52101 ATTTTCCATA CATAAACATT TTCCGTACCT AAACAGTTTG TTTGTTCATT
52151 TGTTTGTTAG TTTGTGTTGG ATTTTCACTC TGTCGCCCAC GCTGGAGTGC
52201 AGTGGCGTGA TCTCAGCCCA CGGCAACTTC TGCCTCCAAA GTTCAAGCAA
52251 TTCTCATGCC TCAGCCTCCC GAGTAGCTGG AGCTACAGGC ATGTGCCACC
52301 ATACCAGGCT AATTTTTGTA TTTTTTTTTA GTAGAGACAG AGTTTCACCA
52351 TGTTGGCTAG GCTGGTCTCA AACACCTGAC CTCAACTGAT CTGCCTGCTT
52401 CGGCCTCCCA AAGTACTTGG ATTACAGGTG TGAGCCACCG TGCCCGGCCT
52451 GTGAACAGTT TTTAGATGAT TAGTAGATAG TAAGACCACT CTTAACCAAT
52501 TCAATACTGA ACATAATTAG TTTTCCTTGA TTACTTGAAA GTACTTGTTT
52551 TTTAATGATA TTAAACATTA TTAAGTCTTG TGAAAATGTG AAATTAGAGC
52601 TTTCTGGGAA TTCTAGATAG AGTTTCCAGT AATAATTAAT GTTTAACAAA
52651 ATTCAGAATT ATGTATGAGG CCTAGAATTA AGACTAGCTT GGGGCTGGGC
52701 GTGGTAGCGC ACGTCTGTAA TCCCTGCACT TTGGGAGGCC AAGGCAGGTG
52751 GATTGCTTGA GGCCAGGAGT TTGAGACCAA TCTGGCCAAC ATGGTGAAAC
52801 CCCATCTCTA CTAAAATTGC AAAAATTAGC CAGGTGGGGG TGGTACGCAC
52851 CTGTAATCCC AGCTACTCAG GAGGCAAAGA TTGTAGTGAG CTGGAGACCA
52901 TGCCACTGCA CCTCAACCTT GGTGACAAAA TGAGACTCTG TCTCAAACAA
52951 AACAAAACAA AACAAAACAA AAAACTAACT TTGGATAGTT TTGAAAATAA
53001 GTAAAACTTC AGAAAGAATC AGAAGGTAGG AAAAACTGCT TATATAGTTA
53051 AATTGTGGTT GGTGAGTATA TTAGTCATTT TATTGCCTTT TTGAATATGT
53101 ATGGCAACCC TATTTATAGT AATTGGGCGT AAGTGAGAGT GTTAATATGT
53151 TTAAGGTTTG GAACATGTAG AAGCTGTTGG TGCCTTATGA AAGTTCTGCA
53201 CCAGCCCCTT AGCAACAAGT GCCTGTGACT TGAAGCTCTT TAATGTACAG
53251 TTGCACATTT TAAGAATCCA AGTTGACTGA TAAATTATCT AATGTATCTA
53301 ATTCAAATAT TTTTAAGAGC TATTGTAATC CCAGTACTTT GGGAGACTGA
53351 GGCAGGCGGA TCACTTGAGG TCAAGAATTT GAGACCAGCC TGGCCAACAT
53401 GGTGAAACCC CATCTCTACT AAAAATACAA AAGTTAGCCA GGCATGGTGG
53451 CGCACACCTG TAGTCCCAGC TACTCAGGAG GCTGAGGCAG GAGAATCGCT
53501 GGAACCCGGG AGGCGGAGGT TGCAGTGAGC TGAGATTGTG CCACTGCACT
53551 CCAACCTGGG CAACAGAGTA AGACTCTGTC TCAAGAAAAA AAGAGTTATT
53601 GATGTTTTGC TTATTATAAG CAGCAATGTT TTGTAGTAAG CCATTTTTAA
53651 ATAGTGAATT TTTTGCTGTA TCAGAATATA GTAGCATAGT AATTTTTACT
53701 CTTATTTAAC TCATAGCAAA GGTTACTCTT ATTTGGAATT CTCCTTTCAG
53751 TTAAATAATT TATACCAGAC TTTCTGAAAA TGTTTGAGGA GGATTATATG
53801 GGTTCTTATT TACTGGTTCT TTGAGAATTT CAAAATACTT TACACATTTG
53851 CTTTATATTC CCATAGCAGT TTAGATAGGG TGTGTTACCA AGATGGAAAC
53901 TGGTTCTGCA GGACTGGTAA CTTATGATGG CCAAACAATG AGTCATTAAT
53951 AAATAGATTT TTGAACAAAG CTTGAAACTG TAATTTCTGC TGCTTTGTGC
54001 TATTACATTT TCAGAAATTT TGACACTGAA CGTATTTTAT TTTTTAAAAA
54051 GTATGTAGAA TGTAGAGAAT GCAAATAATA ATGCTCAGAT GTTAGTTTTG
54101 TCTGTTTCTT AAATTCTTCT GAGCAGAAAT ACCAACCTTG CCAGTACATC
54151 ATGTGTGTTT TCACTTATAT ACAGCCTTCT GTTGGCACTA CTAAAGTTTT
54201 TAAAATGTTT TTTGTTCTCC CCTAGGTGTT GGATCCTGAA CAAAACCATA
54251 ACTTCACAGA TCATTATCTA AATGTGGCCT TTGACCTTTC TCAAGTTCTT
54301 TTTATAGCTA CTGCCAACAC CACTGCTACC ATTCCAGCTG CCTTGTTGGA
54351 CAGAATGGAG ATCATTCAGG TTCCAGGTAC CTGACTCTTA AATCATTATG

FIGURE 3A-17

54401 ATACATCTTG CCTTTCTGAC CATAACTTTA AAATTAGTTA TGCTATGGAG
54451 TTTTGACTAA AAGAAGTTCA TTTGCCAACA TACAATCTTC AGAAGTTCTG
54501 AGGAATGTAT ATAAATCAGT TTCTATGTAG CTTCAAAGTC TGGAAGAGCA
54551 AAACAGCAAA CGTTGACAAC AACAATTTCA GATTTAATTA GCATGAAAGA
54601 ATGATAATTT TATGACAAAT AAGACATTCT TCTTTAGTAT AATTTCTAAA
54651 ATGGCAGGCT GTGTGTGGTG GCTCACACCT GTCATCCCAG CACTTTGGG
54701 AGGCTGAGGC AGGTGGATCA CTTGAGGTCA GGAATTCGAG ACCAGCCTGG
54751 CCAACGTGGT GAAACACCAT CTCAATAAAA ATACAAAAAT TAGCCTGGCA
54801 TGGTGGCGGG CGCCTGTAGT CCCACCTACT CGGGAGGCTG AGGCGGGAGA
54851 ATTCCCTTGA ACCTGGGGAA GGGAGGTTG CAGTGAGCCT CACGCCACTG
54901 CACTCCAGCC TGGGTGACAG AGTGAAACTC CATTTCAAAA AAAAAAAAA
54951 AAAAAGAGTA ACTGAACTTT CTCATAAAAT CTGGCCTCAC TTTTATATTA
55001 AAGTGCATGC CGCTTTTAAA TTCCTCTTGA ATCTGTCAAA TAGTTAAATT
55051 TTTTAAATGT CTTCCCTGTC ACTGGAGCGT GCAAAATGTA TTCCTTCAGT
55101 TACTAACACT AGATAAGTTA TAGCATTTTC ACCTTATTTT AATTGCTCAG
55151 AATTGTTTTT CCCTGGAAGA GATCAAATAT CACTGAGTTT TTTTTTAATG
55201 TAGAGTAGAA TCTAAATGTC TTTATTTATT TAATTATTTA GAGACAGAGT
55251 CTAGCTTGTT GCCCAGGCTG GAGTGCAGTG GCACGATCTC GGCTCACTGC
55301 AGCCTCCGCC TCCGAAGTTC AAGTGAGTCT CGTGTGTCAG CCTCCCAAGT
55351 AGCTGAGATT ACAGGCACTC GTGACCACGC CCAGGTAATT TTTGTATTTT
55401 TAGTAGAGAC CATGTTGGCC AGTCTGGCCT CGAACTCCTG GCCTCAAGTG
55451 ATCTGCCTGC CTTGGCCTCC AAAAGTATAA GGATTACAGA CGTGAGCCAC
55501 CATGTCCAGC CTAAATGTCT TTTACTTATT TTTTCTTTTT TTGAGATGGA
55551 GTCTCACTCT GTCACCCAGG CTGGAATGCA GTGGCACAAT CTTGGCTCAC
55601 TGCAACCTCT GCCTCCTGGT TCAAGCGATT CTTGTGCCTC AGCCTCCTGA
55651 GTAGCTGGGA CTACAGGTGT GCACCATCAC ACCTGGCTAA TTTTTGCATT
55701 GTTAGTAGGG ACAGGGTTTC GCCATATTGG CCAGGCTGGT CTTGAACTCC
55751 TGACCTTAGG TGATTCACCC GCCTCAGCCT CCAAAGTGCT GGGATTACAG
55801 GCGTGAACCG CCACACTCGG CCCTAAAATGT CTTTAGATTC TAAATGTAAT
55851 CTAAATGTAT TTTTCATATT AATCTGAAAT ATATTTTTAC TACTAAGTGA
55901 ATTATAATTG GATTTCTGTT TGTTTTTTTT TTGAGATGGA GTCTCACTCT
55951 GTCACCAGGC TGGAGTGCAG TGGCACGATC TCAGCTCACT GCAACCTCTA
56001 TGTCCCAGGT TCAAACAATT CTCTTGCCTC AGCCTCACAA GTAGCTGGGA
56051 CTACAGGCGT GCACCACCAC GCCCAGCTAA TTTTTGTATT TTTAGTAGAG
56101 ATGGGATTTC ACCATGTTGG CCAGGAAGGT CTCAATGTCT TGACCTCATG
56151 ATCCACCCAC CTTGGCCTCC CAATATAACT GGATTTCTTA ATTATCTGTG
56201 AGCATTGCAG GTTCCTGTAT TTAGTTTTAA AATATGGTAG AGTAAAAAGT
56251 TAATTGTGTG TATTTAAAGT CTAAAGTAAA TAAGTAATGA ATTCCCTGGA
56301 AACTCCAAGT TATGGCAGAA AATTCATTAG ATACACTAAA GTAAAGTGAA
56351 AGAATCAGGA CAGCTGCTGC AGAGGGGAGC ATATGATGCC ACCTTCTTCC
56401 TTTGGCAGAT TTAGCTGTCC GATCTTCTAG CTTTCCTGGT GTTTACTAAC
56451 CTCTTTCCAT TCAAAAGGTG CCTTATCAAT TCATATTTTT AATTTTTGCT
56501 TGTTAAATGG AAAGGGACAT TAGTTGGAAT TTTGTCTTAC GGGATTTAGA
56551 GACAAAGGAA ATCTATATTT ATTCAGGCTA TTAAATAAGA ACATTATGTG
56601 TTCTAAATAT ACTATATATA GAAAAAATAC ATATATACAT ACATAAATAC
56651 ATATGCACAC ATATATAAAT ACATACACAC ACACACACAC ATATATATAT
56701 ATACCATCAT GTGGAGGAAA AAACCTTTTA TATGGACATC TTAGGTTTTC
56751 TTTTGCTGCT ACAATTTATT TTATAGTCAT AGTTCTGGAA ACAGTATCTT
56801 TAGAGCCCTT CCCTTGGAAC CCACTGCTTA TTTAATTGAG GTGTGTGTGT
56851 GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTTT CAAGTATAGA
56901 TCAAATTAGG CTAAAAAGAT GCATTTATTC TTCTATTTGA AATTTCAGAG
56951 GATTTGAGGA TAAAGAGATA ATTGTCTCTA AGATTTGAGG TGTTTTCCTC
57001 TTTGGGAAAT ATATCATTTA ATCAGAAAAC TTTCAAGCAC TGTGCTTAGT
57051 AAATGCTTGT TTTGTTTGTG AAAACGTTGG AAATTTTAAC AATTATTGAC
57101 TTAGATCAAA TTTCTTTTTC TTTTTTTTTT TGGAGGCAGT CTCTGTTGCC
57151 CAGGCTGGAG TGCAGTGGTG CAATCTCAAC TCATTGCAAC CTCCACCTCC
57201 CCAGCTGAAG CAATTCTCGT GCCTCAGCCT CCAGAGTAAC CAGGACTACA
57251 GACATGCGCA ACCATGCTCA GCTAATTTTT TGTGTTTTTA GTAGAGACAG
57301 GGTTTCGCCA TGTTGCCCAG GCTGGTCTCA AACTCTTAAG TTCAAGTGAT
57351 CCGCCCGCCT CAGCCTCCCA AAGTGCTAGG ATTACAGGTG TGAGCTAACG
57401 TGCCTGGCCA GAATAAATTT CTTCATTGTA ATTATAGTCT CATTTGAAAT
57451 AATACTTAAA TTTGTTCTAA ATCTAAGATC CATTTAATGC TACATTTGAT
57501 TCATTAAAAA AGCATGGCAC TGGCTGGGAG CAGTGACTCA TGCCTATAAT
57551 CCTCAGCACT TTGGGAGGCT GAGGNNNNNN NNNNNNNNN NNNNNNNNN

FIGURE 3A-18

57601 NNNNNNNNN NNNNNNNNN NNNNCTATAA TCTCAGCACT TTGGGAGGCT
57651 GAGGCTGGTG GATCACTTGA GGCCAGGAGT TTGAGACCAG CCTGGCCAAC
57701 TTGGCAAAGC CCTGTCTACT GAAAATACAA AAATCAGCCA GCGTGGTTGT
57751 GCATGCCTGT AATCCCAGCT GCTCGGGAGG GTGAGGCAGG AGAATCACTT
57801 GAACCTGAGA GGTGGAGGTT GTAGTGAGCC GAGATCACGC CACTGCACTG
57851 CAGCCTGGGC GACAGAGCAA GACTCTGTCT CTAAAAAAAA AAACAAAAAA
57901 CAAAGCATGG CATTATGGGA GCCATGTAAA TAATTACAAA ACAAGATCTC
57951 TTCTTTTCCA GGTTATACAC AGGAGGAGAA GATAGAGATT GCCCATAGGC
58001 ACTTGATCCC CAAGCAGCTG GAACAACATG GGCTGACTCC ACAGCAGATT
58051 CAGATACCCC AGGTCACCAC TCTTGACATC ATCACCAGGT TAGTTAGCCA
58101 TCCTGAGGCT TCATTAACTC CAGGCAACTT TTGAGTATTT ACTGAGTTAC
58151 CAAACAGGAC ATAGAGTATC AATATTTGAG TTTTTCATCT TTTGAGATAA
58201 GCCACAGTCT CCTGAAAAGG AGATTAGTTT ATTGGCATCC CATAGCATCC
58251 ATTTCTCTTT CTTCAACAAC TTCCAGCAAG TGTTATCATA ACTATTGATT
58301 TACACCGTTC TCTACACTAG GCAGAAGTTT ACAGAGAAAC CATTTGGAAT
58351 ATTGTTATAG CTAAAGCTGA AATTTATGCT TTGCCACAAT AGCAATATAA
58401 GGGGTTAATT TGATCATTTA AAAACCAAAT ACATGGCAAA TATAGAGACA
58451 CTTTTTATGC CCAGGATCTT GAAAGTTGTT GAATTCTCTT AAGAGGTGAT
58501 ATGCTACTTT CAGATAATCT GATTTAAGTT ACTCACTTTT CTTTTCTTCT
58551 CTTTGGCTGA GAGATTTTTA AAATCCTTAG AATTTTGATC TTCAGAATTA
58601 ACACTGGAAC AATAGAGAAG GTGCCTTCCC AAGTTTACTA CCAAATGCTT
58651 AAGCCTGTAG CAAGCAGTGT GTAAATTATC TGAATAGAGT ATTGCTTAGT
58701 CTAATTTACA GATTCCCTGT TTGAATGGAA AATATACTCT GTTGAGAATT
58751 TATATCCACC ACAGCCTCTT ACAGTTTTCC TAGCTCAGTA TTACAGATCC
58801 ATTGCATCAT CCAGCAAGTC ATGTCAGGCT GCCAAGCTCT CCTCTTGCGG
58851 CCCTTTTCTA GTAACTACTG TTTTTAAGAG ATTTGAAGTA TCTCTCTATT
58901 TTGAACTTTG ACTTAGAGTT TGGCCAGACT GTCTTTTGAT CTATGCCTTC
58951 TTATGGATCT ATTTAGATTT ATATACAAAG CAGTAAGACT AAGTCTTACC
59001 TGGGGGTTCC TTTTCTTAAT TTGTCTTGTG ATTTATGGTG TAGATAATGC
59051 CAGGAGAAAT AAATTAAGTG ACTTATATGT CTGAGTCTTC CAACAATATC
59101 ATTATTCCAG ATAACACCCA TGATGCCTTT GGGTAACTTT CAATAAGTCA
59151 TTTAACATTT TTGATAGCTT CCCCATCTGT AAAATATGAG GGATGGAGAA
59201 AAATCCAGAG TTTATCTGAA TAATAATGAT TCTGAAGAGT GATCATTATT
59251 TATATTTCCC AGTTGTTACC TAGAGAACTG TTTCTTTTTT TATGTATACT
59301 TGTTAACTCA AAATATCAGA TCTTAAAAGC TGTGGACATA AGGAAATATC
59351 TGGAGCAGTT TTGTTAGTTT TGATATTGTT TTTAAAAACA GCACAAGTAT
59401 GTACTATTCC AGGCACAGTT TTTGGATATT TAGTGAGTTA CCAAACTTAG
59451 GACATAGAGT ATCAATATTT GAGTTTTTCA TCTTTTGTGA TAAGTCACAG
59501 TCATAGACCC TAATGTTCTA GTCTTTCTTA TCTCCAAGTA TAACTCACCT
59551 GCTTGAATAC TTCCAGTCCC AGTATGCTTA ATTCTAGCGA ATAACTACCT
59601 TTTCATGGGT AATTCTAACT GTAACAAAGA TATTCTTTTT ATTTATTTAT
59651 TTATTTTTTA AGACAGGTTT TCATGCTGTT ACTCAGGCTG GAGTGCAGTG
59701 GCATGATCTT GGGTCACTGG AGCCTCTGCC TCCTAGGCTC AAGCCATCTT
59751 GCCATCTCAG CTCCCAAGTA GCTGGGACCA CAGGTGCATG CCGGGCGTGG
59801 TGGTGTGTGC CTGTAATCCC AGCTACTCGG GAGGCTGAGG CAGGGAATT
59851 GCTTGAACCA GGGAGGTGGA GGTTGCGGTG AGTTGAGATC GTGCCACTGC
59901 ACTCCAGCCT GGGCAACAGA GTGAGACTCC GTCTCAAAAA AAAAAAAATA
59951 GAGATGGGGT TCTCACCATC TTGGCCAGGC TGGCCTGGAA CTCCTGAGCT
60001 CAAGTGATAA TTGTTACAAA GATACTCTTT CTATTCACTT TTCTATAATT
60051 TTCTTCTTCT GCCTTATAGG AGCACCTGGA ATCTAAGTGT AATTCCTCCT
60101 TGTACAGCCC TTCTGACATT AAGATAAAAT ACTATCAGGT GCTGCACACT
60151 AAGTGTTCTC TTCTTCAAGC TAACCATTCC TCTCCTCTGT ACCATTCCTC
60201 TTGATGTAGT TTCAAGACTT CTCACCCTCC TGATTAGTCT TCTTCTGAAA
60251 GAATCCTGTA TATCAATGTG TCTTTTAAAA TTAAACACCC AGAATTGAAC
60301 ACAGTGTTTC AGATAGAGTC TAAACAGTTC ATGGTATAGG AAGCCCATGC
60351 TTTTCTTATT CTGACTATAT TATTTTATGA CTGTATCTCT AGATTCTTAG
60401 CTTTTTAAAG ATTATTCTCT TCCCTTTTTC AGTGAATTTC GCTAAGCTTG
60451 GCATATCCCA TTTTGTATTT ATAAAGCTGA ATTTTTTAAA GCCCAAATGT
60501 AGAAGTTGTT AAGATGCCTC CCTGTTTTCT CCCTTATTGA AATTATACGT
60551 AGTTGCATAA TATAGGCTTT ATATCCTTCT ATACCTTTGA CTGAAATGAG
60601 TATTAGAGTG TTTAGCTAAG AGCTTTTTAT CTGTCTTTTC TCAGAACTTT
60651 TAAAATCTGC TTTCCTAAAG TCTACAGTGT ATGTCTGACT TAATCAAATG
60701 TATGGCTTTG TCAAATCCAA TTCTTCAGAT AAAACTGCAT TCTCCACCTG
60751 ATCCTGTCCA TTCAGGTCCA TCCAAAGCTG AGTGGCCAAA AGTGGTTTCA

FIGURE 3A-19

60801 CTATATAATG GTCTGTGGAA TGACTTAACG GAGTTTGATT CTAATGTACA
60851 TGTGTTTAAA GCAGCTCTGC TTAAACCACA CATAGCATCT TTTTCACAAA
60901 GTCCTCAAAG TCAGTGCTGT CATCACTTAG CATACCTTCT TCCTTTAGAA
60951 ATCTTCACAA TGAAAATACA CTGAAGAAAG GTGGTTAGCA AAGTGCCTAG
61001 TGAAAACCAG ATTTCTGTCT CAGATTTGTT TTTGTTTTAG TTCCACAAAG
61051 AGCACAATTT CTCTTATTCT TTCAGTAGTA TTTCAAATAC AATGAATTTA
61101 TCTAGAATTT TCCTAAATTG ACAAATTTTG TTTAAGAAAA CTCTTCAACA
61151 AATTACCGAG GAGTAAATGG TTTTTTATAT GCTGCCAAGT TTACTTTGGC
61201 AATGTAAATT GAACTAGAAC TAGGGTTCAT TTTTAAGTGT AGGATTATAA
61251 TTCAAGATAA TCTGTATAAA GGAAATTGTT GTAGCTGAAA ATAGATCAAA
61301 GTATTGAAGA AATAACAATA ATGAGGAGTT TTAAGTGTGG AAAAGTTAGT
61351 ACTCAAGAAA GGGTAATGAA CTTTTAAATG TACACTGTTT TACCAAAAAT
61401 GTTAATCACA TTACCTCTCT ATTTTTTTAA GTGGTATATA GTCAAAAATA
61451 AAATATTTTT GTTTGATGAC AGGTATACCA GAGAGGCAGG GGTTCGTTCT
61501 CTGGATAGAA AACTTGGGGC CATTTGCCGA GCTGTGGCCG TGAAGGTGGC
61551 AGAAGGACAG CATAAGGAAG CCAAGTTGGA CCGTTCTGAT GTGACTGAGA
61601 GAGAAGGTTG GTGACCTTGT TCTGGCATTC TCAGGCCTGG TGGCTAGGAG
61651 TGAGTGACAG AAGAAGGTTG GGTATGGAGG GGAAGGTGTT GGGTAGTCCT
61701 TGGAGCAGTG GCACACATGA CTCCACTGTT AAATGCATCC AGTAAGTAAT
61751 ACCTTAATGT TTCAACATAT TTCATCCAGA GGATTGTCTT TTACAAATAG
61801 CACAGTTTTA ACTGGAATAA TAATATGAAT GCTTTGAGGA TATAGGAACT
61851 GTATTAGGGT TCACTAGAGG GACAAGACTA ATAGGATAGA TGTGTATATG
61901 AAGAAGAGTT TAAGGAGTAT TAACTCACAC AATCACATGG TGAAGTCCCA
61951 CAATAGGCCA TCTGCAGGCC GAGGAGCAAG GAAGCCAGTC CAAGTTCCAA
62001 AATCTCAAAA GTAGGGAAGC CGACAGTACA GCCTTCAGTC TGTGGCCGAA
62051 GCCCCAAGAG CCCCCAGCAA ACCACTGGCG TACGTTCAAG AGTCCAAAAG
62101 TTGAAGAACT TCGAGTCCAA TATTCGAGGG CAAGAAGCAT CCAGCACGGG
62151 AGAAAGCTGA AGGCCAGAAG ATTCAGCAAG TCTGATCCTT CCAGCTTCTT
62201 TTCTCTGCTT TATTCTAGCC ATGCTGGAAG CTGATTAGAT GGTGCCCACT
62251 CAGATTGAGG GTGGGTCTGC CTCTCCTAGT CCGCTGACTC AAATGTTAAT
62301 CTCCTTTGAC TATATCCTCA CAGACACACT GGAACAATAC TTTGCATCCT
62351 TCAATCCAAA GTTGAAACTC ACTATTAACC ATCACAGTAA CTTTCTCCAG
62401 ATGTATAATG ATGGTGTACG TTATGTATGG GTTCTGGTGT TATCTTATTT
62451 CTTTCTGACC CAGACAGTTA AGTCTTTAAA TAATTTATAA CATAAAAAGT
62501 TTTTACAACA TAAGACAATC CATGCTGTTC AGGTACTGCA AGGACAGACC
62551 TTTGTACTCT GGAATAGCTC CATGTGTAAT AATTTTTCAC ACATTTTCTT
62601 TTATGGATAA ACAACTAAAT GTAATTTAAA TTATTCTTTA AAAAATTATT
62651 GTGAAGGTGT TCTATTACTG GAATTAATCA AATGTGGATG TTCCTTTGGT
62701 ATCTACTTAA AATGTTTTAA CTGGCCAGGC ACAGTGGCTC ATGCCTTTGA
62751 TCCCAGCACT TTGGAAGGTT GAGGCAGGCA GATGACTTGA GGTCAGGAGT
62801 TTGAGACCAG CCTAGCCAAC ACGGTGAAAC CCCGTCTCTA CTAAAAATAC
62851 AAAAATTAGC CAGGCGTGGT GTTGGGCGCC TGTAGTCCCC GCTACTCTGG
62901 AGGTTGAGGC AGGAGAATCG CTTGAGCCCA AAAGTCAGAG GTTGCAGTGA
62951 GCAAAGGTCA TGCCCACTGC ACTCCATCTG GGCAACGGAG CGAGACTCCA
63001 TCTCAAAAAA ATAAATAAGT AAATAAAATA AAATGTTTTA ATTTCTTGCC
63051 CCAAAACTGT AAGGGGTCTC AGTTCATCAT ATCATGCTGT TATGCAGTTT
63101 GCCAAAACTT GCTTTAACAA ACATGAGTTG TAGGGAATTG ACAATTTCTT
63151 TCATAGTAAA GAGATTTATT AGATTTTTCT ATCATTTCCA TAGCTGTTTC
63201 CAGAAAGGAG TTGGATGACT GTGATTAAAG AACCATAATT TATGGTGGAC
63251 CCAGTTGAAC AGACACAGCC AAATGTCTTT CTTGTTTTTC CATCAGTCGC
63301 TGAACACAGT GCATTTTACA GCAGTAGCAT CAGAGTCAGC TTTCACAGAA
63351 TCCTTCTGTG GCCAGTACAG TGCTTCACCC CTGCCTCCCC ACGCCTGGAA
63401 CCTCACTGGT TCATTTTCTC CAGAGAGCGA AGCTCCTATC TTCTGTTGGA
63451 TTGGAGGGAG GCAGTGCCTT CATTATGTGG AGTAGGAGTA GAGGTAGTGA
63501 GTTCTAATTG TATTTTATCC AGACTTTAAA ACTTGTGCTT TATTTTTATT
63551 ATTTTTATTT TATTTTACTT TTTGAGATGG AGTCTCGCTC TGTCGTCCAG
63601 GCTGGACTGC GGTGGCACAA TCTTGGCTCA CTGCAACCTC CGTCTCCGAG
63651 GTTCAAGTGA TTCTCCTGCC TCAGCCTCCC CAGTAGCTGG TACTGTAGAC
63701 GGATGCCACC ACGCCCGGCT AATTTTTGTA TTTTTAGTAG AGACAGGGTT
63751 TCACCATGTT GGCCAGGCTG GTCTTCAACT GCTAACCTCA GGTGATCTGC
63801 CCACCTTAGC CTGCCAAAGT GCTGGGATTA CAGGTGTGAG CCACTGCGCC
63851 TGGCTTTATT TTTATTTTTT ATTTTTACTC TGCCTTGGGA GAATCTAGAA
63901 AACTTTTGCC TTTTGTCCCA CTCTTCATCC ATGCTTTCAG GGCTACCTTG
63951 AATTCTTTAG CTTTTGTAGA CTTTTAGGAC CCACATCAAC TTGTTGTTCT

FIGURE 3A-20

64001 CTATCTCTAG CCCCACAAAT GTTGAGGTTT CTGCTTTCTC TAGCCTGTTA
64051 AGTGTTGGTT ACTTTTTGTC CATGTACTTT TTGTTTCCCA AAATTTTGTC
64101 AGCATCTCTT GTCAGCTGAT GTCCTCTTTG TCATTATTTT TGTTCTTGTG
64151 GGTTTATATA TTTTTTATTT CTTAATTGTC ATTTTAATAC TATTCAGACA
64201 GGAAGTAAAA ACGCATGCTC AGACTACCAT TTATAGAAAT TTGAATTTAA
64251 AAAAAATGTC CTAGGTGAGG GAGTACCTAT CAAGGGTGGA AATCACTTGT
64301 GTAGATGACA GTGACAGTGG AGAACTGAAG TCTATAAAAG TTAAGACCTA
64351 GATCTAGATG CTCCTGAATT TCCCCTTTTT ATTCTTAACA ACACTTCCTT
64401 TGTGCTGTGA TCTCAAGCAA CTGAGCCTAG GTCTTTTTAT TCTTGTCTGA
64451 TATAACAGAA GGTAGAGGAT GAAATAAATG AGTTTATTAG GTAACACATT
64501 TTGAAAATTG TGTTTAAGAT TTAGATGATA TATTTTAGAA CTTCTAATAA
64551 ATTCAGAGGA ATTCAATGTC AAAGGAAACT TTTGTATAGT TATACATTGC
64601 TTAATGTTTA TACATACATC CATGTAGCAT ACTTCTAATA ATATCTTTAA
64651 TTATACTAGT TATTTTAAAA TAACCCACAA ATACTCAAGG AATTGTTCAG
64701 TTTGTGAACT GTGTGAGAAC TACAGTTTTT CATGGTAACA TTTATTTGTG
64751 TGGTTTTTAA AAGTGATCAC AGGACATCTC CTAAAAGATA ATATAGTTAA
64801 GCAGATTTGC TTAGTTAAGA TATTACCAAG AGCATCTAGA TGAATAATTA
64851 GAATAAATAC TTGTCTCTTG GAGACGATTT TGGGTGTAGT CTTTACTAGA
64901 GGCATAGGTA TGGACTCCAA GTTGGCTCTA ATATTATGAG ATACCCTTGA
64951 GTAAATAACA GCCATTCTCT AGACCTTAGT AGAATGATTA TTAGGTGTCC
65001 TGAATTGTTT ATGACCTCAA CCAAACCAAA AGAATAATTT CTACAAAAGA
65051 GTCTATGTTA GGTTTTCATA GCACCAAGTT CAAATGGAGC TTAGTAATGA
65101 AAATTTTCTC ATTAAGAAAT GAATTAATTA AAATTAAGAG CATAAAATAA
65151 GACAGTTGTT TTAGAAACTT CAAGTAATAC AGTGTGGGAG TTATTTTTAA
65201 TGTTAAAAAT AAAGCTTTCC TAATTCAAGC ACGAGAGACA GAAAAAAAAT
65251 AATAAGGCTG AACTTGGAGT TACTGCCAGG AAGAAAAGTA ATTTTAGGCC
65301 ACAAGCTTCA AAACAGGCAG AAACCTCCAG TGTATCAAAC AAACTTTCTG
65351 GAATAGGCCC AGAAGCACTG ATCTGTGAAC AGTTGTCTTT GTATTTGTGG
65401 GGTCTTAACT GGCAGTTAAA GAGACTAAAT AATAGCAGGG AGTTTAAAAA
65451 GCAGGTGAGA TTTAGAATTG ATCGATCTGT GTTAGCGGAG GAACATTTAT
65501 GGTTTCAGTC ACTTACCTAT AAAGTATGAG AATTGTTTCT TTAAAAGAAT
65551 GCTGCCTCTG TTTTTCTGCA TGTTGTTAGT ATTTTCTGAA TTGCCGTTTT
65601 CCTTTCTAGG GTATTTGTTG GGTTGAGAGA TTAGTTGGAT TACATGACTA
65651 CAGTTTTATT CTGCTTTTTG CCTGCCTTTT GCCAAGAAAG ACACAAATGT
65701 CCCATGTATT TAATTTTGCA CACTTCAGTG TTTCTAAACA GGGTAAATGT
65751 TCATTTGTTT AAGTACCCAT GTATCATATA TTCAATTTAT ATCTAGCAAG
65801 ATTTTTCCTC AAAAATTATC CTAAGCAAAG AAGGATTTAT ATTATAATCA
65851 GTCCTTATAA AGTTTCTCAT AATACACTGC ATTCTCAATT ACTTTATTTT
65901 TGAAGAACAT AGTATTTGAG GAAGTTACAT TAAACAGAAA GAACCTGGGT
65951 AGATACTAGT TTCTGATTAT TTTCATAGAA GTCACCTGAA AAATTGGTTA
66001 GAAAAAAAAG ACAAAATTAA TACAAATTTA ACAGTTATTT GTGAAATATG
66051 TAAATGTTGT GTTATTCCAT TTTGCTGTGC TACAAAGGAA TACTTGAGGC
66101 TGGGTAATTT ATAAAGAAAA GAGATTTGTT TGGGTCAGAG TTCTGCAGGC
66151 TCTATAACAG GCACAGTGCT AGCTTATAAG GTGAGACCTT AGGTAGCTTA
66201 TAATCATGAT GGAGGACAAT GGGAGAGCAG GCATGTCACA TGGTGAGAGA
66251 GGGAGCAAGG AAAGAGCCAG GGACCTTTTA ACAACCAGCT GTCATGTGAA
66301 CTCATTACCA TGGGGAAGGC ACCAAGCCAT TTATCAGGGA TCTGCCCCTG
66351 TGACCCAAAC ATCTCCCAGT AGGTCCCTCC TCCAACATTG GGAAACAAAG
66401 CTATAGTAAC CAAAACAGCA TGGTACTGGT ATAAAAATAG ACACATAGAT
66451 CAATGGAACA GAATGCAGAA ACTAGAAATA AAGCCACAAA TCTACAGCCA
66501 ACTGATCTTT GGCAAAGTAG ACAAAAACGT ACACTGGGAA AGGACAACCT
66551 ATTCAGTAAA TGGTGCTGAG AAAATTGGAT AGCCATCTGC AGAAAGAATG
66601 AAACTGAACC ACTCTCTCTC TTATTTTATA TAAAAATCAA CTCGAGGTTA
66651 GGCTAGGTGG CTCACACCTG TAATCTCAGC ACTTTGGGAG GCTGAGGTGG
66701 GTGGATCACT TGAGGTCAGG AGTCTGAGAC CAACCTGGCC AAAATGGTGA
66751 AACCCCGTCT CTACTAAAAA TACAAAAATT AGCTGGGCGT GCTGGTGCAT
66801 GCCTATAGTC CCAGCTACTC GGGAGGCTGA GACAGGAGAA TCACTTGAAC
66851 CCAGGAGGCG GATGGTGCAG TGAGCCGAG ATCGCGCCAT TGCACTCCAG
66901 TGTAGGGGTA TCGCAGCGAG ACTCTGTCTC AAAAAAAAAA AAAAAAAAGT
66951 CAACTCAAGA TAGATTAAAG ACTTTAAATG TAAAATCCAA AACTAAAACA
67001 TACTAGAAGA AAATCTAGAA AAAATTCTTC TAGACGTTGC CATAAACAAA
67051 GAGTTCATGA CTAAGACCTC AGAAGCAAAA GCAACAAAAC CAAAAGTAGA
67101 CAGATGAGAC TTAATTAAAC TAAAAAGCTT TTTATACAGC AAAAGAAACA
67151 ACAGAGTAAA CAGACAGCTT GCAGAATAAG CAAAAATATT TGCAAAATAC

FIGURE 3A-21

67201 ATATGCAAAA GACCAATACC CAGAATCTAC AAGGTAACTC AAGCAACTCA
67251 ACAACAACAA AAGAACCCCA AATAACCCCA TTAAAAAGTA GGCAAAGGAG
67301 ATGAAAGACA TTTTTCAAAA GAAGACATAC AAGTGGCCAG GAAGCATTTG
67351 AAAAAATGCT CAATATCACT AATCATCAGA GAAATGAAAA ATCTATGAGA
67401 TACCATCTTA TACCAGTCAA AATGGCTATT TTTAGAAAGT CAAAAGTAAC
67451 AGATGTTGGT GAGGATGTGG AGAAAAGGGA GTGCTTATAT AGTGCTGGGA
67501 GAAATGTAAA TTAGTACCAC CTCTATGGAA AACATATGGA GAGTTCTCAA
67551 AGAACAAAAA ATAGAACCGT CATTTGATCC AGCAATCCCA CTACTGGGTA
67601 TATACCCAGA GGAAAAGAAT TCATTATGTC AAAAAGATAC CTGCACACAT
67651 ATGTTCGTTT TATCTGATAT AAAAAGTCTG TTTTATCTGG TATAAAAAGA
67701 ATGGAATCAT GCCTTTTGCA GCAATATGGA TGAAACTGAA GGCTGTGACA
67751 ATAACTCAGA AATTCAAATA CTGAATATTC TCATTTATAA GTGGAAGCCA
67801 AATAATGTGG ACATATGAAC ATAGAGTGTG GAATAATAGA CACAAGCATG
67851 AGCTATCATG CCCAGCCTCA AAAAATTTAA TTTCCCTCTT AATTTTGTCA
67901 TTGACCCAAA GGTTGTCCAG GAGCATGTTG TTTAATTTAC ATGTGTTTGT
67951 ATATTTTTGA GAGTTTCTCT TCAGATTGAT TTTTAGTTTT ATTCCATTGT
68001 GTGAAGATAC TTGATATGAT TTTGATTTTT TTTTAAATTT ATTGAGACTT
68051 GTTTTGTGGC CTGACGTTTG GTCTGTCTTG GAGAATGTCC CATGTGCTAA
68101 TGAGAAAAAT GTATCTTTTG TGGTTGTTGG GTAGAATGTT CTGTAAATGT
68151 CTGTTAGGTC CATTTGGTTT TAAGTTCAGT GTTTCTTTGT TGACTTTGTC
68201 TGTCTCAGTG TTGAAGTCCC ACATTTTGTA TTGCTATCTG TCTCTTTTCT
68251 TAGGCCTAGT AGTATTTGTT TTATTAATCT GGTACTCCAG TTTTGGGAGT
68301 ATATACTTAG GATTGTTATA TCTTCTTGTT GAATTGATCC CTATGTCATT
68351 ATATACTGGC CTTTAAAAAA AAAAAAACTA TTGTTGATTT AAAGTCTGTT
68401 TTATCTAATA TAAGTATAGT TACTCTTGCT TGCTTTTGGT TTCCTTTTGC
68451 ATGGAACATT TTTCCACCCC TTTACCTTCA GTCTGTGTGT CTTTAACAGT
68501 AAGGCAAATT TCTTGTAAGC AGCATGTAGT TGTTGTTTTT TAATCCATTG
68551 CACCAATTTA TATCTTTGAA GTGGTGCATT CAAGGTTAAT ACTGATGCAT
68601 GAGGTTTTGT TCCAGTCATA ATGTTAATTG CTATCTAGTT GCTTTGTAGA
68651 TTTTTTTTTT TCTTTTAAGC AAGAGTCTTG AGTCTTGCTC TGTCACCCAG
68701 TCTGGAGTGC AATGGCGCGA TCTTGGCTCA CTACAACCTC CACCTCCCAA
68751 GTTCAAGCGA TTCCCTTGCT TCAGCCTCCC AAGTAGCTGG AATTACAGGT
68801 GCATGCCACC ATGCCTGGCT AATTTTTGTA TTTTTAGTAC AGACGGGATT
68851 TTGTCACGTT GGCCAGGCTG GTCTCGAACT CCTGACCTCA GGTGATCCTC
68901 CCGCCTTGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAA CCACCGCAAC
68951 CAGCCAGCTT TGTAGATTCT TTGTTTGTTT TTTGTTCCCG CTTGTGGTC
69001 TTCTGGAGTT CTGTCATGTT GCCCTTTTAT TTCTTTCTTT TCCTTATTTG
69051 TATAATTGTT TCATAAAACT TGTGAGTTTC ATGTGTTTTT ATGATAGAGT
69101 ATCACCTTTT GTTCCCATGT TTAGAACTTC TTTAAATATT TCTCATAGGA
69151 CCAATCAAGT GGTGATGAAT TCCCTCATTT GCTTATCTGG GAAACACTTT
69201 ATTTCTCCTT CATTTGTGAA GCTTACACTA GCAGGATACA AAATTCGAGT
69251 TTGACCATTT TCTTTAAGCA CTTTGAAAAT AGAATCCCCG TCTCTTCTGG
69301 CTTCTGAAGT TTCTGCTGAG AAGTCCACTG TTAGTTTGAT GAAGTTTCCT
69351 GTATAAGTGA CTAGACACTT TTACTGTATT TAGGGATTTT CCCTTCACAT
69401 TGACCTTAGA CAGCCTGATG ACTAGATGCC ATGGTGAGAT CCTTCTCGCA
69451 ATGTATTTGG CTGGAGTTTG TTGAGCGTCT TGTATCTGGA TGTCTAGATC
69501 CTTTGCTAGA CTAGGGAAGG TTTTCTCAAT TATTTTCTCA AATAGGTTTT
69551 CTGAAATTTT TGCTTTTTCT TCTCCTCTAG GAATACCTAT GATTCATAGG
69601 TTCCAATGTC TTATGTAATC CCTTACTTTT CAGAGGCTCT ACTCATTTTT
69651 TAAAATTCTT TTTTCTTTTT TTTTTTTGTC TGACTGGATT AATTGAAAAA
69701 ACCTATCTTA AAGTTCTGAG GTTCTTTCTT CTGCTTGGTC TAGTCTGTTG
69751 TTGAAGCTTT CAAATGTATT TTATAATTCC TTCAATGAAT TTTTTATTTC
69801 CAGGAGTTCT GTTTGGTTTT CTTTTTAAAA TACCTATCTC TTTGGTAAAT
69851 TTCTCATTCA TTTCCTGAAC TGATTTTCTG ACTTCTTTGT ATTAGTTTTC
69901 AGATTTCTCT TGTATCTTGT TGAGCTACTT TTTTTCTTTT AATTTAATTT
69951 TATTTTGAAA CAGGGTCTCG CTCTGTTGCC TTGTCTGGAG TGCAGTGATG
70001 CAGTCATAGC TCATTGTAAG CCCAAGCAGT CCTCTGCCTC ACTGTCCTAA
70051 GTAGCTACAA ATTCAGGCAC ATACCACCAC ACCTAGCTTA TTTTTTTATT
70101 TTTTGTAGAG ATGGAGGGTT ATACTGTGTT GCCCAGGCTA GTCTTGAACT
70151 CCTGGCCTTA AGTGATCCTC CTTCCTCTTG CCTTGGCTTC CTAAACTATT
70201 GGGATTGCAG GCATGAGTCA CTGTGCCCTG CCCCTGACAG CTTCTTCTTT
70251 TTTTTTTTTT CTGAGACAGA GTTTTACCCT GTCACCCAGG CTAGAGTGCA
70301 GTGGCACGAT CTCGGCTCAC TGCAGCCTCC ACCTCCTGGG TTCAAGTGAT
70351 TCTTGTGCCT CAGCCTCCTG AGTAGCTGGG ATTACAAGCG TGCGTTACCA

FIGURE 3A-22

70401 TGCCTGGCTA ATTTTTGTAT TTTTTTAGTA GAGATGCGGT TTCACCTTGT
70451 TGGCCAGGCA GGTCTTGAAC TCCTGGCCTC AAGTGATCCA TCCACCTTGG
70501 CTTCCTAAAG TGCTAGGATT ACAGGTGTGA GCCACTGTAT CCAGCCCCTG
70551 ATAGCTTCTC TAAATCAGTG TTTTGAATTC TTTATCTGGC ATTTTGAAGA
70601 TTTGTTTTTT AGTTAGGATC CATTGCTAGA GAATTACTGT GTTTCTCTGG
70651 GGGTGTCATA GCACCTTTTT TTTTTCATAT TTCCAATATT ACTGTGCTGA
70701 TTCATTTGTA TCTGGGATAA CAGTTGCTTC TTATTATTTT TTAGTTTACT
70751 TTTGTTGGGG CAGGACTTTC TTTCCCTTGA GGATGTATCT ATTATGTATG
70801 TTGAGTAGGG TCATTTGGCT TTGCTTCAGG GTGCATTCAG TGACATAGAC
70851 ACTGTATGAT AGCCTTGGTT ATAAAGTAGT CTTAGTATGG TGGCTTTCTC
70901 AAATGCCAGT GACAGTAGTA ATGTACGGGG TGGGTGATTG GGCTCAAGGC
70951 CTCCTGCCTA GCTGGGGTGG ATGATGGTGG CAGCAGAGGT CGTGCAAAAC
71001 TTGCTTTCTT CCAAGGCACT ATGCAGTTGT ATCAATAGAT GTTGTAATGG
71051 GTGGTGCAGG TTGACTTCCC AGCTAGGAGG TGGTGCCTGC AGATGAGCGT
71101 CAGCTGCAAT AGTGGCAGTA GGGTGATTAA CCTTTGTAAT TCAAGAATTA
71151 TTCAGGTATC TCAGGTACCG AGCTGGGCCG TGAAACTCTC AGGGGTCCTG
71201 GTCTTGTGCT GTGCTTCCAG GGTAGATTGT GGGGTGAAGC CAGGCAGGCT
71251 GGACCAGCCA AGCTCATGTT TGAGCCCCCT GAATGGGTAC TTAGGGCCTG
71301 GGATAAAATT TCCAGAGGCT GCCTCATACA TTGTTTCAAG AATTACTTTA
71351 TCTTAGATAA TCTTGGTATC TGGTAGTGTA AGTCTTCCAG CTTTGTTCTT
71401 CTTCAGAATT GGGTTGGCTA TTGTAGGTCC TTCAAATATC CATGTAAATT
71451 TTAAAGTCAG TTTGTCATTT TCTACCAACA AGTAAATAAA TAAAAACTCC
71501 TGGGGCATTT TTATTATGAT TCCGTTGAAT CTGTAAATCT AGTTGGGGAG
71551 AATTGACAAT TTGTATTATC AAGTCTTCTA ATTCATGACC AGCTTCATTT
71601 ATTTAAGTCT TCTTACATAA GTTTTTTTTC TTCAGCTTTT AAGTTCCAGG
71651 GTACATGTGC AGGATGTACA AGTTTATTAT GTAGGTAAAC ATGTGCCATG
71701 GTGGTTTGCT GCACAGATAA TCCATCACCC AGGTATTAAG CCCAGCATCC
71751 ATTAGCTATT CTTCCTGATG CTCTCCCTCC CCTCACTCCC ACCCACAACA
71801 GGCCCCAGTG TGTATTTTTC CCTGCCATGT GTCCATGTGT TGTCATTGTT
71851 CAGCTCCCAC TTATAAGTGA GAACATGCAG TGTTTGGTTT TCTGATCCTG
71901 CATTAGTTTG TTGAGGATAA TGGCTTCTAG TTTCATCCAT GTCCCTGCAG
71951 AGGACATGCT CTCGTTCCTT TTTATGGCTG CATAGTATTT CATGGTGTAC
72001 ATGTACCACA TTTTCTTTAT CCAGTCTGTC ATTGATGCGC ATTTGGGTTG
72051 ATTCCATGTC TTTGCTATTG TGAATAGTGC TGCAATGAAT ATATATAAAT
72101 CATTCTGTTT CTTTGGCTAT ATACCCAGTA GTGGGATTGC TGGATCAAAT
72151 GGTATTTCTG CTTCTAGATC TTTGAGGAAT CACCACACTG TCTTCCACAA
72201 TGGTTGAACT AATTAAACTC CCACCAACAG TGTAAAAGCA TTCCTTATTC
72251 TTCACAACCT CGCCAGCATC TGTTGTTTCT TGACTTTTTA ATAATTGTCA
72301 TTCTGACTGG CGTGAGATGG TATCTCATTG TAGTTTTTAT TTGCATTTCT
72351 CTAATGATCA GTGATGTTGA GCTCTTTGTC CTATGTTTGT TGGCAACATA
72401 ATGTCTTCTT TTGAGAAGTG TCTGTTCATG TCCCTTGCCC ACTTTTTAAT
72451 GGGGTTGTTT TTTTTTTTCC TTGTAAATTT GTGTTCCTGG TAGACTCTAG
72501 ATACTAGACT TTTGTCGGGT GGATAGATTG AAAAATTCTT TTCCCATTCT
72551 GTAGGTTGTC TGTTCACTCT GATGATACTT TCTTTTGCTG TGCAGAAGCT
72601 CTTTAGTTTA ATTAGATCCC ATTTGTCAAT TTTTGCTTTT GTTGCTATTG
72651 CTTTTGTCAT TTTCTTCATG AAATCTTTGC CCGTGCCTAT GTCCTGAATG
72701 GTATTGCCTA GATTTTTTTC TAAGGTTTTT ATAGTTTTGG GTTTTACATT
72751 TAAGTCTTTA ATTCATCTTG AGTTATTAAA TAATTTTTGT ATAAGGTGTA
72801 AGGAAGGGGT CCAGTTTCTG TTTTCTGCAT ATGGCTAGCC AGTTTTCCCA
72851 GCACCATTTA TTAAATAGAG AATCCTTTCT TCATTGGTTA CTAGTACAAA
72901 AACAGACACA TAGACCAATA GAATAGAATG GAGAACTCAG AAATAAGACC
72951 ACACATCTAC AACCATCTGA TCTTCTTAAA TAAGTTTTTT AAGAGTTTTG
73001 ATCATTTTCT GTGGCACACT TTTACATAAT TTTTCTTTAG ATATCTTCCT
73051 AGGTATTTGA TCTTTATGTG TATATTATTG TAAATAACGT TCTTAAAATT
73101 TTGTTTTCTA ATTTTTTGTT GGTAGTGTAT GACAATGCAA TATTGGCCTC
73151 CTGTTCAACA AACTTGCCAC ATTCACTTAT TAATCATAAT TGTTTGTGGA
73201 ATCTTTTGGA TTTTCTGCAT CTACCATCCT GTAATCACAA ATGCAGATGT
73251 CAGTTTTTAC TTCTTCCTTT CCAACGTTAT ACCTTTTATT TAATTTCTTC
73301 CCTAATATGT TGGCTAGGAC CTCCTGGGAA ATGCTGAATA GAAATAATGA
73351 TAATAGACAA AGTAAGCAGG ATAAAAGCCT ATGAAGAAAT TACCAACTGA
73401 CATAGGCTTT GCTTTGTAGC TTTAGGTCAC CCCTCATCAC CTAATATTAT
73451 AAAATGACAA TTCGGTAGGA TTCTCAGAAA CTGTCCAGTT TGACCCTGAT
73501 TTAATTCTCA ACATTCTCCA GTAAACACTA TGCCTTGCCT GTTTGACTTT
73551 GTTAACAGAC ATGTCAGACA ATCATGTGGT GAAGTGTGAT TTTACTTGTT

FIGURE 3A-23

73601 TATTCAACCT GAGATTTGCT GACAGTTCGT TCTGTGTTGC TGTAACAGAA
73651 TACCACAGAC TGGGTAATTT TAAATGAGCA GAAATGTATT GGTTCACAGT
73701 TCTGGAGGCT GAAGAGTCCA ATGTCAAGGT GCCAGCTTCT GACAGGAACC
73751 TTCTTGCTGC ATCTTCACAT GGCAGAAGGG CAAAGAAAGA GAAGGGGCCC
73801 TGAACTCACT CTTTTATAAG GATATCAGTC TCACCCATAA GGGCAGAATC
73851 TTCAGGAACC TAAGAGCAAC TTGTTACTTC ATGGCCTACT GACCTCTTAA
73901 AAGTCTCACT ACTTAATATT GTTACAATGG CAGTTAAATT TCAACATGAA
73951 TTTTGAAGGG GACAAACATT TAAACCATAG CACTGACTTT CTTGAATTTG
74001 TATACTCTTT TATTGGTTTT GGAAAGATTT TGGCCATTAT CTTTTCAAAT
74051 ATTCTTCCCA TTTTTTTACT CTTCCTTCTG GGATTCTGAG AAGAGAGCCC
74101 TTCACTGTCT CTTATCCTCC TTTCTATTTT TTTTTTGTTT GTTAATTTTT
74151 CTCTCTCATT CAGTTTAGAT ATTTTCTGTT GCCCTGTATT CCAGTTTGTT
74201 ATTGCTTTCT TCTATTTTTT TGTGGTCTGC TATTAAGCCT ATGAAGTTCT
74251 TAATTACCAT ATTGTAATTT TTTTTTTTT TTTTTTTAC TTTTAGAATG
74301 GCCACTGGAT ATTTTTTTTT TCTTTCTTTA AGACAGAGTC TCACTCTGTC
74351 ACCCAGGCTA AAGTGCAGTG GCACGATTTT GGCTTACTGC AACCTTTGCC
74401 TCCTGGATTC AAGCGATTCT GATGTCTCAG CCTCCTGAGT AGCTGGGATT
74451 ACAGGCGTGT ACCACCATAC CCAGCTAATT TTGTATTTTT AGTAGAGACG
74501 GGGTTTCACC GTGTTGGCCA GGCTGGTCTC GAACTCCTTA CCTTAGGTGA
74551 TCTGCCCTCC TCTGCCTGCC AAAGTGCAAA GTGCTGGGAT TACAGGCATG
74601 AGCCACCGCG CCCAGCCCAT TGGATTCTTT TTTTTTTTT TTTTTTTGA
74651 GACGGAGTCT CGCCCTGTTG CTCAGGCTGG CATGCAGTGG CGTGACCTTG
74701 GCTAACTGCA ACCTTCACCT CCCAGGTTCA AGTGATTCTC TTGCTTCAGC
74751 CTCCCGAGTA GCTGGGATTA CAGGCGCCCG CCACCACACC CGACCAATTT
74801 TTGTATTTTT AGTAGAGACG GGGTTTCACC ATGTTGGCCA GGCTGGTCTT
74851 GAACTCCTGA CCTCAAGTGA TCCACCCACC TTGGCCTCCC AAAGTGCTGG
74901 GATTACAGGC ATGGGCCACC ACACCCGGCC AGGATTCTTT GTATATATAT
74951 GGACTCCAAT AGATTCTCCA TTGATATTTT CTATCTTTTT ATCTATTTAA
75001 TCCCTCCTTT TCCCTATTTT CTTGGACATG CTAGTCATTA TTTTGAAAAT
75051 CTCTACCTTA ACACTCCATT ATCTGATTCA GTTATGTTTG GTGTTTGTTT
75101 TGTTTGTATT ACCTTTTTTT CCCCCTTGAT TTCTAGTTTT TTGTTCTGTT
75151 TTTTAGCATT TCTTGTATTT TTTTACTGGA TGCCAGACAT TGGATGAAAA
75201 ATACAAGGGC TGTAACTATT ATCCTCTGAA AAGTGTTACA TTTTCTTCTG
75251 ATTGGTAACT ACAGTACCAA CCTGTCACTC TGTCCTGTCA AGGCTGAGTT
75301 TTAGGCTTTG TCAGGACTCG TCAATTTCAG TTTGGGTCTT ATTACTGGGA
75351 TACAGTCTTT ATTTTTATTA TGTGGTACTC CCAGGATGTA GTTCTTATTC
75401 CTTGGTGGGT GACCCTTACT TCTAGAGCAT GATCTTTCTG AGTTCTCACA
75451 TGAAAATCCA ATCAGGTCTT TAGCATCCTG GCTTCTCCTT TCTCCTGGGT
75501 TTCTAAAAGA CTCACCCTGA ATACATTCAA CTTAGGAGTT AGTCAACAGC
75551 TTGAGGGGGA TTTAAGTGCA GATTTTTGAG ATCCTTCTTT TTGGTTTCTT
75601 CCTTTATTGG GATTTTGCCA ATGAAGTCCC AGTTGCTTTG ACAACCTCTA
75651 ATTTTCAGAA TTACTTTTGA CTAAATGTTT TATGATTCTA AACATACCAT
75701 CTACTCTGTC AATTCTGAAT TATGGTGATA CTCAATTCTA CCTCAAATCC
75751 CAAAGAAAAG AGGGGGAAAA AACAACAAAA CTAAGAAGAA ACATTGCTTT
75801 TGTTTTGTAG CTTTAGGCTT CTACCTATAT AATTGACTAT TATAAAATCT
75851 CATTTGAGTA GGATCTTTAG TAGCCACCTA CTTTGACTGT GATTTGATTT
75901 ATAAATCCCT TCACAACATT CCTCAGTAAA CACCATGCTT TGCCTGTTTG
75951 ACTTGGTTAA CAGACATGTC TTTATAAACT TGGCTATCCA TTTTCCAGTC
76001 TGTAGGAAAA GAGAAGCTGT AAGTTGGAGA AAAGGCTAGT GGTTGGGTGG
76051 TGAGTCATAA GCAATAAGAT TTGATGTCAG TGATGACAGG CCTGTCCTCT
76101 TATGATAGAT TCCTTGAGCC CCCTGCTGAC CACAAAGCTT TGGCTGGCTA
76151 GACCACAAGT CTGTCTCCCT CAATGACAAT TTTTGTAGCT CAATATGGAT
76201 CCTATTTTGT GTGAGTTGCA TTTGGAGATT TATTGTTTAT CTGCTGTATT
76251 TGCCTTAGGT GGGACAGTGA AATCAACCTA ATGTAGTGGA AGGAAGTAGG
76301 TATTACATCC TTAATTCCTT GATATACATC CTTTTATTAT GTGGTACTCC
76351 CGGGATGTGG TTTTTCAGAT TTGGAGAAGA ATAGTTAAAA AAAAAAAATG
76401 CAGAAAGGAT CAAAAGCACT TGATTCTCTC GCAGGGACAG CTTCCTGTTT
76451 TGGTTGAGGA AGGAGCTGCA CTTAAAATAA CTAGCATAAA GCATGCTTAG
76501 GGCTTGCTTT CCAGACAACC TCAATTTAAA ATGCATCAAA AGCCAGGTGT
76551 GGTGGCTAAC ATCTGTAATC CCAGCACTTT GGGAGGCTGA AGAGGGCAGA
76601 TCACTTGAGG TCAGGAGTTT GAGACCAGCC TGGCCAACAT GGTGAAACCC
76651 CATCTCTTCT AAAAATACAA AAATTAGCTG GGCGTGGTGG CACACACCTG
76701 TAGTCCCAGC TACTTGGGAG GCTGAGATGG GAGGATCATT TGAACCTGGG
76751 AGGCGGGGAT TGCAGTGAGC CGAGATCACA CCACAGCACT CTAGCCTGGG

FIGURE 3A-24

76801 CAACAGAGCA AGACTCTGCC TCAAAAAAAG AAAGAAAATA AAATTCATCA
76851 AAATAAAATA TTTGAATTTT ACAGCACTAG TTCTTTTCAT TCATTGACTT
76901 TCATTCTCCC ACTTTACCAC ACCTTTAACT ATTGGCAAGA ATGTGGTGAG
76951 TGGGAGAAAG CGTATCCTGC CACGTAAGCA AGTATACCTA GAGCCAAGGG
77001 GTCAGAGTGT CACAGAGGAG AGCCACATGC TGATGGGCTT GTGTTCGTTC
77051 CCACTCACTG ACTATGCAAG CGCCTCTTCT CTTAGCCTTT CTCAGGATGC
77101 AGTTCTCCAG GGAGGAATCA GCCTTCTGTT GGGCTGCTTT CAGAGCTCTT
77151 TGTTGTGGCT TCCTGCCATT GACTTTGCAA GCCCTAAGCA TGCTTTATGC
77201 TAGTTATTTT AAGTGCAGCT CCTTCCTCAA CCAAAACAGG AAGCTGGCTC
77251 TGCAAGAGAA TCAAGTGCTT TTGATCCTTT CAGCTTTTTT TTTTTTTGAC
77301 TATTCTTCTC CAAATCTGAA ACATATCCAT TCTCGTCTAC GGCCATGAGT
77351 GCATTTATGT TAACAGAAAA TGCTAAATTT AATGTTTAGA AAGTAACCTC
77401 TGTGGCCAGA CATGGTGACT AATGCCTGTA ATCCTGGCAC TTTGGGAGGC
77451 CGAGGCAGGC AGATCACTTG AGGCCAGGAG TTCGAGACCA GCCTGGCCAA
77501 CACAGTGAAA CCCTGTCTCT ACTAAAAATA GAAAAAATTA GTTGGGCATG
77551 GTGGTGGGTG CCTGTAATCT CAGCTACTTG GGAGGGTGAG GCAGGAGAAT
77601 CACTTGAGCC CAAGAGGTGG AGGTCGCAGT GAGCCAAAAA TCAAGCCACT
77651 GCACTCTAGC CTGGATGACA GAGCAAGACT CTCTCAAAAA AAATAAAAAG
77701 TAACCTCTGT GCTTTGTGTA ACTTTTTGCT AAATTCCTGT CTTTGTCTTC
77751 TTGGAACAGT CTTCTACTTG TTACAGGATC TTCCTATCTT TTGGATTTTA
77801 TATTAGTTTT AATATAAAAT TAATATAGTT TTATATTATA TAGCCCACTG
77851 ACATGGCTGT TAGCTGACCT CAGTTCCTTG CTGACTTGGC CAGAGCCTTC
77901 AGTTTCTTAT CTCTGGTAAG AGGTAATGTG TCTCTCCCTA GGGCAAGGCT
77951 GTGACAGCTG GCTTCTCCCA GAGGGAATGA TGTGTGAGAG AAGCAGGGAG
78001 AGTAAGAATC AAGACAAAAC TGCAGTCTTT TATACCCATC ACTATTGCCA
78051 TATTCTCTTG GTCACACAGC CCAACCCTGG TATGATATGG GAGGCACTAA
78101 CTCCATGGGG ATGGGATATC TGGGCACCAT CTTGAAGGCT AGCTGACACA
78151 GATTATTTTT TGTGCGTGTG CCTGTAAGAA TTTTTTGGCC AGGCGTGGTG
78201 GCTCACGCCT TTAATCCCAG CACTTTGGGA GGGCGAGGTG GGTGGGTCAC
78251 GAGGTCAGGA GTTCAAGACC AGCCTGGCCA AGATGGTGAA ACCCCATCTC
78301 TACTGAAATA CAAAAATTAG CCAGGCATGG TGGCAGGGGC CTGTAATCTC
78351 AACTACTCGG GAGGCTGAGG CAGGAGAATC GCTTGAACTT GGGGGCGGA
78401 GGTTGCAGTG AGCCGAGATC ACGCCACTGC ACTCTAGCCT GGGCAGCAGA
78451 GTAAGACTCT GTCTCAAAAA AAAAAAAAAA AAAAAGAATT TTTCTAAGCC
78501 CGCATTGAAG TTTATACTGT AGAATATCCA TCAAACTTGA GCTGATTTCT
78551 TATCAAAGAC CCAGGTTGCA CAGATAGGGG TTAGAAGTTT GGATTCGGTT
78601 TTGCATTTTC AGTATTTAAA GTCTTGTTTC ATCTTGTTCA TTCTTACCTT
78651 TCCTTTGATT GTATTAGTAG CTCAGGACAA ATAAGAATTT ATAATTTTCC
78701 AAGGAACTAA GGTTGCTGTT GAGGAATATG GGTTTCAGAG ACAAGAGTTT
78751 AGGCACTGGC TCATTGGTAC TAAGCTTCAG GGGTTTGTAG TGTTGTTAGA
78801 GCTAATTGGA TTTTACAAAT AAGCCAAGAT TATTAAAAAA AAAAAATAGA
78851 TCTAGAGAGT AACACTTTCT GTGCTAAATC CATTGCATTT GATGGGATAC
78901 TAGGCAGTAT GCTATGTCCA AACTTCTAAA ATCAGGCGGT GGTCTAACGT
78951 TGAGGTGAAA ATATCATGTT GGGTATATAC TGCCAATATC ATGAAGATAT
79001 ACTAAATATT ATTTTCTGAG TCTGACATTT ACACTGATTT ACTGATTTAT
79051 CCCTCATCAA TATTGGCCTG GTTTAAGAGA GACTTGTTTG CCTGTACAGA
79101 CCGGGAGGAA GCTTCAATGA AGGCAAAAAT CTAACTATAA TAGGAGCCAA
79151 ACATTTGTTA TTTGAATTCC AATTGGGGAC AGGAAAATAA AATATTATCA
79201 AATAATTATA AAGTCATCAT TCTGTTAAAT GAATCATATA GGAAAATGCA
79251 TTGACCTTAA AACAGAGTCT GGCTCTGTTA CCCGGACTGG AGTGGAGTGG
79301 CCTGGTTTCA ACTTGCTGCA ACCTCCACCT CACGGGCTTA AGCTGTCCTC
79351 CCACCTCAGT CCCTAGAGTA GCTGGGACCA CAGGTTTTGC CATGTTGCTC
79401 AGGCTGTTCT CAAACTCCTG AGCTCAAGAA ATCCACCTGT CTCAGCCTCC
79451 TGAAGTGCTG GGATTACAGG CGTGAGCCAC CGCGCCCGGC CTGCAGTGAC
79501 CTTTGGTTGT CATTGTTATA CATTATCAAA ACAAACTCAA GTTACAAGAG
79551 TATTAAAGCA ATACTTAATG GTTTTAAAAA AAATATTACA AAAGGTCTCT
79601 GCATTTTAAC TACTCATCTA AATAATTGTC TAGGAATATT TTCTGAATCT
79651 CTAATACAGG AAATGAGATT TATTAATACA TAAAACCCAC TGAAAACAGG
79701 GGTGCAAACT TTCTTGTCTG GTACTAAAGA TGGATTCCTA TGTTTTGGGC
79751 CCTTGTTTAT ACCAGTTTAT TCAATCAGTG AGTCAGCTAG CATTTACTGA
79801 ATAGTCATAT GCGTTGCTTA ATGATGGGGA TAATGTTCTG AGAAGTGCAT
79851 CCCTGGGAAA TTTTGTCATT GTGGAAACAT CATAGAGTGT ACTTACACAA
79901 ACCTAGATGG TATAGCTTTC TACACACCTA GGCTATATGG TATAGCCTGT
79951 TAATCCTAGG CTATAAACTT CTACAGCATG TGACTATACT GAATACTGTA

FIGURE 3A-25

80001 GGCAATTATA ACAGAGTGGT ATTTGTATAT CTAAACAACA GATGAACAAT
80051 AAAGAAAAAA TAAACAACAA ATAAAAGCTG GTACTTCTGT ATAAAGGCAC
80101 TTACCATGAA TGGAGTTGCA GGACTGGAAG TAGCTCTGCG TGAGTCAGCA
80151 AGTGAGTGGG AGTGAATGTG AAAGCCTAGG ACATTACTGT GTATATACTA
80201 CTATAGACTT ATTAACACTG TACACTTAGC CTGTATTTTT TAATTTTTTT
80251 CTTTTTTTTT TTTTACTTCT TTTTCTTTTT TTGAGACAGG CTGTGTTGCT
80301 CAGGCTGGTC TTGAACTCTT GGGCTCAAGT GATCCTTCTA CCTCATCCTC
80351 CTAAGTAGCT GGGATTACAG GTGTGTGCCA CCACACCCAG CTTTTTAAAA
80401 CTTTTCAAAT CTTTTATAAT AACACTCAGC TTAAAACACA AATACACTGT
80451 ATAGCTATAC AAAAAATATT TTTACCCCAT TTATGCCTAG TGCTCCATTA
80501 TTGGAACACT AAGCTTGTGG GAGTTATTTA TATCCTACTG CTCAAGGTCA
80551 TTGCCAAGGT CTGATTTTTC ACAAAAAAAA ATTCACAACT TCTGGCATAA
80601 ATGGGTTAAT ATCCTTACTG TATATAAGCT TTTTTAAAAA TTGTTTTACT
80651 TTTTAAACTT CTTTGTTAAA AGCAAAGACA CAGACACACA TTAGCCCAGT
80701 CCTGAACTAG GTCAGGATCT TCAGTTTCAC TGTCTTCCAC TTCCACATCT
80751 TGGCCCACTG GAAGGTCTTC AGAGGCAGTA ACATGCATGG ATAACAGTGC
80801 CTTCTACCTT CTGAAGGACC TGCCTGAGGC TGTTTTACAG TTAACTTCTT
80851 TTTTACAGAA GGGAGTACAC TCTAAAATAA TGATGAAAAG CATAGTATAG
80901 TCCAGGCACG ATAGTGTGTG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG
80951 GCAGGAAGAT TGCTTGAACC CATGAGTTCA AGACCAGTCT GGGCAACATA
81001 GCGAGACTCC ACCTCTAAAA ATATATATAA GAATAAAAAA TTTTTTTTAA
81051 ATGAAGCATA GTAAGTACAT AAACCAATAA CATAGTCACT CACTATGACT
81101 ATGAAGTATT ATGTACTGTA TGTAATTGTA CGTGCTGTGC ATTTATACAG
81151 CTGGCAGCAC AATAGGTTTG TGTACACCAA GCATCACCAC AAAGATTTGG
81201 GTAATGCATT CCATTGCCCT AACGGGGCTA CAACATCACT AGGCAATAGG
81251 AATCTTTCAG GTCCGTTGTT GTCTTCTGGG ACTTCTGTCA TATATGTGGT
81301 CTGCCTTTGA CCAAAATGTT GTTATGCAGT GCGTGACTAT ACCCACTATA
81351 TGTTCAAGTT CTAAATTGGA TTCTGGGAAG CTGATTAAAG AGAAAATAAT
81401 GTGTAGTCTA TTGGAAGAGG TAGATAAACA ATTTTTAAGT GAAATAATTG
81451 CTAATTTTTA ACCTCTGTGG AGGCACTGAA CTGATCATTG AAAGCTCTAT
81501 TTTACTTACT AAAGATATGG TAGCTTATAA AAATTACTTA TAGTAAATGG
81551 ACATGAAAAG GTCATTTGCT TACATCTCTA AATTCATTTT GATGGAAAAA
81601 TAGTGGAAAA ATGTTTGCAG ATACCCTTTT GTTTGTTTGT TTTTTTCATA
81651 ATAGATAATT GCCACTAAAA TTGAAGAATG GCCAGGTCCG TTGGCTCATG
81701 CCTGTAATCC CAGCACTTTG GGAGGCCAAG GCGGGTGGAT TACTTAAGCT
81751 CAGGAGTTCA AGATTAACCT GGCCAACATG GCAAAACCCC GTCTCTACTA
81801 AAAATACAAA AAATTAGCCA GGTGTGGTGG TGCACACGCC TGTTGTCCCA
81851 GCTACTTGGG TGACTGAGGC ATGAGAATCA CATGAGCCTG GGAGGCGGAG
81901 GTTGCAGTGA GCTGAGATTG TGCCACTGCA CTCCAGCCTG GGCAACAGGT
81951 GAGACTCTGT CTCCAAAAAA AAAAAAAAAC AACTAAAATT GAAAAATACC
82001 TCACAGTCAT AACTTCCATC TGTATCTCAG TGGTTATTAT GTAGAAATGT
82051 TCAGTAGGTA AACTTGAAAG AAAATGTATT TGGTAATCGT AAGGTTGTGT
82101 TGCCACCCCC AAAATAATGA AGAAAATACC AACAGAAAGA AAAAGGATTT
82151 ATTGCTGGCC TGAAGGTTCT TCTGGGCATT TGATCTACAG ATTTCTCCAT
82201 TATAGCTAGT TCCTTTAAAA AAATAAAAAA CATTGAAAAT ATGCAGACCC
82251 AAATGCCTTG GCAGCCCTGG TCAGTAACTT GAATCTCAGT TGCACTTAGC
82301 ACAATTCCTC TGGCTGGGAA GATGTTGTTT TGGAAAAGAT TAACCTGAAA
82351 TGACAGCACG AATTATACAG TTGGAAATAC TCAGGTTTTT CTGATTTTTT
82401 TCAAAAGATA CTTTGCTTTT CCTTTTCTGC CTTACCATGG GAAGGTCCTT
82451 AGATGCATCA TATCCTTGTC AGTTTAGCCT TGTGACACAT ATTTCTGCAA
82501 TTTTGTGCAA TAAGAAAGCC ACTCGAAATC TCAGCATTTC ATGTCACTTT
82551 TAAAGTAGGC TCAGTTAAAA CAAAACCACT TGATTGTTTG TATAACCACA
82601 ACCATATGTG TCTTTCTCTC CATGCTTAAA CAAGGTCTGA AATCGTGTGT
82651 CAAACAGTTG AGATGTAAAC ATCTCCTCCT CACACATAAC CCCTCTGCCA
82701 TGTTGTTATT TATATCCCCA GTAACACACT TCTTGTCCCT GACACAAGTA
82751 CAGCCGTCTC CACATTCCAT TTTGCTCCTA CTCCATCAGC TTGCAAGAAA
82801 AATTTTAATC ATTCAAAAAT AATTGTTACA TAATTACTTT TCACTGATTA
82851 AAAATATTTG TTTACTTGAC AAAATTAGCA TTAAAAACAG TAATTCTTTG
82901 GCAGATTAAT AAGTATTTTG ATGATTTGTC ATTTTTCACA GATGTTGATA
82951 AAATTTAAGA ATTACATAGC CGAAATTTGG TCTAATTCAA CAAACCACAA
83001 TTGACTCTTT TGGTAAGGCC CTATGACGAA TGGTATGGGA GAGTGGAGTT
83051 TATCCAATCT GACTTTCATT TTATTGATAC GGAAACTGGG GCCCCATTTG
83101 TTCTTTTTTT TAATTGCTAC ATAATATACA TATTTATGGG GTATAGTGTG
83151 ATGTTTCAGT ACATGTATAC ATTGTGTAAA AATCAAATCA GGCTGTTTAG

FIGURE 3A-26

83201 CATATCTGTC ACCTCATATA TTTATCATTT CTTTGTGGTA AGTATATTTA
83251 AAATTCTCTA TTCTAGCTAT TTTGAAATAT ACAATACTGT TAACCATAGT
83301 CACTGTGCAA TAGAACAGTG GTCCCCAACC TTTTTGGCAC CAGGGACCAA
83351 TTTCATGGGA GACAGTTTTT CCACGGACCT GTGGGGTGGT GGTTTCAGGA
83401 TAAAACTCTT CCACCTCGGA TCATCAGCAT TAGATTCTCA TAAGGAGCAC
83451 CCACCCTACA TCCCTCACAT GCACAGTTCA TAATTCACAA TAGAGTTTGA
83501 GCTCCTATGA GAATCTAATG CCGCTGCTGA TCTGACCGGA GGCGGTGCTC
83551 AGGCCGTAAT GCTTGCCCAC CCGCTGCTCA CCTCCTCCTG ACAGGCCATG
83601 GACTGGTACT GACCAGTCCA CAGCCTAGGG TTTGGGGACC CCTGCAGTAG
83651 AACACCAGAA CTTATTCCTC CTATTTATCT GCAATTTTGT ACCCATTGAC
83701 CAATCTCTCC CCATCCCCAC TATCTCTCCC CTTGCCAGTC TCTTGTAACC
83751 ACTGTTCTAC TCTCTGTTTC TGTAAGATCA ACTTCTTTAG ATTCCACATA
83801 TAAGTGAGAT CATGCAGTAT TTGTCTTTTG GTGCCTGGCT AATTTCACTT
83851 AATATAATGT CCTCCAGGTT CAACCATGTT GCCACATGTG ACAGGATTTT
83901 ATTCTTTTTG TGGCTGAATA ATATTCCATT GTTTATATAT GTCACATTTT
83951 CTTTATCCAT TCATCCGTTG ATGGATGCTT ACGTTGATTC CATATATTAG
84001 CTATTGTGAA TAGTGCTGCA ACAAACATGG AAGTGCAGAT ACCCCTTTGA
84051 CATATTCATT TCCTTTGGAT AAATGCCCAT TTGTGGGATT GCTGGATCAT
84101 ATGATAGTTC AACTTTTAGA TTTTGAGAAA CCTCCATACT GTTTTCCATA
84151 ATGGCTGTAC TAATTTACAT TCCAGCCACC AGTGTGTAAG AGTTCTCCTT
84201 TCTCCACATC CACACCAACT ACAGGTGGCT TTTCTAGACT GGACTTTAGG
84251 TTGGGACAAA AAGTGTCTTT GAGAGTCAGT AGTCCTAATA CTGTACTGTG
84301 AATGCTGTGG ACTTAGGCAG TTTGTTTAAG CTTGTTTAAA CTGGGTCTCT
84351 CTTTCCTTAG ATATAAAATGG AGGGTTAGAC TGGATCTTTA AGCTTCTGCC
84401 CAGCATTTAA TGTTCTGTTT ATTGTGGTTC TAGCCTGTGC TTCTTGAATT
84451 CCTGATTCTT CCTGAATTCT GCTAAGCATC AGAATGCAGT CTATACATTC
84501 TCAACAGCTT CCCAAAGACA TGATATTAGT ATAACAGAAA CAGTAGTAGT
84551 CCTTTCTTGG AAAATTATCC CCATTTCTGG ACCCTATTTT ATTGCTGGCT
84601 GCAATTAACA GGTTCTTGTA TGTCCCATCC TTCCCTCCTC CTCCCTAACC
84651 CACAGGCATT AAAAACCTGC TGTTTGTGAA AATGAACACT TCTTTGATAA
84701 TCTGGAAGAA GGGGTTCCTG TTACCAGAAA ATTTAGCTCT TGAACTCCTG
84751 GGACTGGGCT TGAAAGCATA GTACTATTAT GCTTCAGATT AAGCAGGGTA
84801 TAGAGAATAA GGAGTGATCA CAAAAATTCT GTCTTGAATA AAGATGATGA
84851 TAGATATCCC AGGGCCCTCT GTGGTTAGAT AGTCTCCATT TCTACCACAT
84901 TCTGAGGAAT TGTGGGTGTT GCGCTTTTTA TGTTTCTGGC CTCCCTGCTA
84951 CTTGCCATTG GTTGGATCAC TGGCCAAGAG CTACCGAGAA CTACCATTTT
85001 GCTTCAAGAT TTTTTCAAAC AGCAAGGAAC TTTTTTATTT TTTAACAGAG
85051 AGCTACTGAA GTTTCCTGAG TTATTACAAC CCCCTTATCC TTCCTCCTTA
85101 CTTCCCCTTT CAATAATTCC CTTTCCTCCC TCTTCCCACA GCAGTTCTTT
85151 GGCTATTGGG CCTGTTTTCA TTGAAATCAT CTTCCTGTGG CAGAGGGAAA
85201 ATGAATAGAG AAGAACAGTT GACTGTGTCC AAGTGATAGC TGCTTGCTTA
85251 GGAAAAGCCT GGTCCTTCCC CAGAGGAGTC TGTCCCTATA GGACTTCCCT
85301 CCATAATAGC TGTGCTTCCA TCAGCTCTAG AGGATGGCTT AGCCCCCTTC
85351 GGGGGTACAC CGCATTTCAC TCTCACTTGG CTCACAGCCA TCACCACAGT
85401 CCATGCTGTG AGTGCATTGC TGGTTCTGCC CCCGTGCTGT GTGCATCTCT
85451 GCTGCTTTAA TGCTGGGAAA CTCCGTGGTT ATGCCCCAAC TATCTTGGCA
85501 ATGTTCTGAA TCAGACATAG ATAATACCTA TTAAAGGTAT TAATAGGCCA
85551 ATAATACCTA GTAAAGAAGA GCTGGGATAT ACCTCTGCAT AGATTAAATC
85601 AACTAGAAAA CACTAGCCCC CTCCCATTTT CAGACCGATT TTATTTCTTT
85651 TAAGTGGGAA AATAGTCGAA GTGGGATGAA GCAGAGCTAG CTTATTCTAC
85701 TCATTTTATA TTTCTGTGGC CTTTTCAACC TCTGTTTAAC AGCACTTTAT
85751 TACTTAGTTT TTTTGTTTTG TTTTGTTTTT TTGGGATGGA ATCTCACGTT
85801 GTCGCCCAGG TTGGAGTGCA GTGGCATGAT CTCGGCTCAC TGCAACCTCC
85851 ACTTCCCGGG TTCAAGCGAT TCTCATGTGT TAGCCTCTCA AGTAGCTGGG
85901 ATTACAGGCA CCTGCCACCA GGTCCGGCTA ATTTTTGTGT TTTCATTAGA
85951 GATGGGGTTT CACCATGTTG GCCAGGCTGG TCTCGAACTC CTCACCTCAG
86001 GTGATCTGCC CGCCTCAGCC TCCCAAAGTG CTGGGATTAT AGGTGTGAAC
86051 CACCACGCCC AGCCTCACTT TATTACTTTT AAGAATATGC TTCAAAATAG
86101 TTTGTAAAGA AGATTTTAAT AGGGAGCACT TATATGAAAT ATAATAGTGA
86151 TATATAGTAT AGCATAGAGC AGAGTCTTCA GTCTTTGTAT CTTTTTCTTT
86201 TTTTCTTATG CATATTTAAT GTATGTGATT CCCAACCGTT GTGTGATTGT
86251 GGTCAGAGCC CTGTCTGTGG GATGCTGGGT AGAATGAGAT TGTAGAGAGC
86301 ACTTTGTTTT CTTGTAATTG AAGGGTTTGG GGTGAGAATA TGTGAGTCAT
86351 AGAAATCTGT ATAGTAAATA TTACTCTAAA AAGGGAGCCA TCAGGATCTG

FIGURE 3A-27

86401 GGAGAATTTG CTAAAGGAAA ACTAAGAATG AAAAAAAGGC CAGGTACAGT
86451 GGCTCACTCC TGTAATCCCA ACACTTTGAG AGGCCAAGGC AGGAGGACCT
86501 GAGGCCAGGA GTTCAAGACC AACCTGGCCA ACATAGTGAA ACCCCGTCTC
86551 TACTAAAAAT ACAAAAATTG GGCCGGGCGC GGTGGTTCAC ACCTGTAATC
86601 CCAGCACTTT GAGAGGCTGT GGCGGGTGAA TCACGATATC AGGAGTTCGA
86651 GACTAGCCTG ACCAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA
86701 ATTGGGCCGG GCGCAGTGGC TCACACCTGT AATCCCAGCA CTTTGAGAGG
86751 CCGTGGCGGG TGGATCACGA TATCAGGAGT TCGAGACTAG CCTGACCAAC
86801 ATGGTGAAAC CCCGTCTCTA CTAAAAATAC AAAAATTAGC CAGGCATGGT
86851 GACGTGTGCC TGTAATCTCA GCTTCTCAGG AGGCTGAGGC AGGAGAATCA
86901 CTTGAACCCA GGAGGTGGAA GTTGCAGTGA GCCGAGATCA CACCATTGCC
86951 CTCTAGCCTG GGTGACAGCG GGACTCCGTC TCAAAAAAAA AAAAAAAAAA
87001 AATTGGCCAG GTGTGGTGGT ACACACCTGT AATCCCAGCT ACTTGGGAGG
87051 CTGAGGCATG AGAATCGCAT GAACACAGAC GGCAGAGGTT GCAGTGAGCT
87101 GAGATCACAC CACTACGCTC CAGCCTCTGT CTCAAAAAAA AAAGGGGGGG
87151 AGGGGCGGTG GGGGGAGCGG GAGCCAGTAT ATAATTCAGT ATCTCTCATC
87201 TATACATATT AAGGCTTTTG ACCATTACCA AATTCTCCCA GCAGCTCTCT
87251 GAGAGTACTG TAATTCTGGT TTTGCTGATT AGAAAACCAG ATACAAAGAG
87301 GTAAAGTCAC CTTGTTCTAG GCCACTAGGT GGTAATCTGA GTCAGGACTG
87351 GAGACAATGA TTTATTTTTA ATATCTCATG TAATGTTAAT CTCATAACTC
87401 AGGGCATAAC TCTTTTACCA TTTTGGACTA TATCATTTCA TTCATATGAT
87451 AAAGACACTG TAGCTTCCCC CTCACCTGCA GCTTCACTTT CTGCAGTTTT
87501 AGTTACCTGT GGTCAACCAT CGTCCAAAAA TATTAACTGG AAAATTCTAG
87551 AAATAATCCA CTCGTAAGTT TTAAATTGTG CACTATTCTG GGCAGTGTGA
87601 TGAAATGTCG AGCCATCCTG CTCTGTGTGA CCCTGGACAG GAAGCCTCTC
87651 TTTGTCCAGC ATATCCATGC TGTATGACTC CCGCCCCTTT AGCCACTCAG
87701 CAGCCATCTC ACTTACCAGA TCAACTGTCT TGGTTTCAGG GTGTTTGTGT
87751 TCAAGTAACC CTTCCTTTAC TTAATAATGG ACCCAAAGCC AAGAGCAGTG
87801 ATGCTGGCAT TCTGGGTTTA TTTTATTAGT ATTGTTGTAA ATCTCTTACT
87851 TTGCTTAATT TATAAATTAA ACATGATCAT AAGTACATAT CTATAGGGAA
87901 AAAATGGTAT ATATAGGGTT CTGAACCATC CTGCATTTCA GGTATCCACC
87951 GTGGGTCTGG AAATGTATCG CCTGTGGAGA AGGGGTGACT ACTGTGTATG
88001 TAAAAATCAC CCTGTGTGAA ATGTTATATC CTCCCCTTTC CTCAGTTTAA
88051 CGTTGTTTTG AAAGAATTTT CTCACATTAC TTGAAAACAC TTAGGAAACC
88101 ATTTTTAGTG ACTGTAGTAT TTTACCAGTT AGATATGCCA TGGTTTACTT
88151 AACCATGTTC CTAATGTTGG GTACTTATAT TGGATCTAAG TTTTGCTGTT
88201 ATTTGTAGTG CTGCGATGGG TGACTGTGCA CAAACCCTTG CCTGTACTTT
88251 TGTGTATTTC CCTAAGGATA GATTGCTGCA AAAAGAACC ACTGAGTGTG
88301 AGACTGTAAA TATTTGGAAG GCTTTCAGTC TATTTCCATA TTGCTTTCCT
88351 GAAAGATTGA ACCAGTTTAT ACTTCTGTAA GCAACAGTGT TTGAGAAGAT
88401 CTCTTTACTT TTTTTAACAT TGACCTTTGT CATTTCTTAA ACTTTACTAG
88451 TTATTTTGGT AACCGGCTTG TTTTTATAAT TTGAATTTCT TTGCTTCTCA
88501 GTGAAATAAT AGTTTCTTTT ATAGGAGTAT TAACCATTTG TTAAGAACCA
88551 CTATTTTAGT CCAAAAGAAA GGTATATAAG AAGAAAACTG CACAATTCCA
88601 GTGGGAAGGA CTTGGGGTCA GGGTCCCTGA TATGTTGGAA GGTTGAACTT
88651 TTTGTTGTTG GTTTTTCCCC TTGCCTTAAA AAGTCCATAT TGCTTGAATG
88701 TTGCAATCTT GGGCAAGGCC AGCAATTAAT CCAAGGGATG ATGCCACTGT
88751 CTTCTCCTGG TGCTGGTCCT TTCTGACAGA GAACATGGTA CTAGGGCTGA
88801 GTGCTTGAAT GCTTGCACAT AGGACCCAGA AGGTGCACAT ATAACCGGGG
88851 GTTCGTTCCT TGAGTGATAT CTTTGTGAGA TGACATTTTG CTTGTTGGTT
88901 GTTTGTTTTA TAATGAGGAA TCAAAGTGGG TATTCTAGGA AGATCCAGTG
88951 TTTCCCTACT CACACTTTGC ATTACACACA GTCCAGGGGG TGACTCAGAA
89001 TCCAGTGCTG TCCTGCCTCT CCCAGTTGGC TGACACCATT TTCTTGACTG
89051 GAGCCTTAGT TTTCTAGGCA TATATTCTAA TGATGGAACA TTTTGAAATG
89101 CAGATTATTT TTGAGGTTAC TGAATTTTTT AATAACACAG CTGCTGTCCC
89151 TAAATTGCCA TCTTTTATAA GGTCTAGTTG CATTAGAAAT AGCTCTCCCA
89201 ACCCCACTCC CCCAGTGCTC AGAACGCTGA ACCCCGTACT ACACTTGGAA
89251 AAGGATTGGA TGTCCTAAAG CATTGGTTAT GTAATTGTGG GTTGGCTTTC
89301 ACCCACTGAG CTTTACTTCC TCCTGTGATC GTGAAATACA AGCTGGCAAC
89351 AGTAATTAGA TCTCAGAAAA GCTTGTCACA AAGCACCACA GACTAGAGAA
89401 ACTTGTAAGC TCTTTTTGCA CTGGCTGAAG TTTTTGAGTA CCACTACCTT
89451 CCATCTATAG TGTAGTAACC TTAGACAGGT AGTGCTTTTC TTCTGTGCAT
89501 TAATTTTAAT TAAGCAATGA CACCTACTTT CTTTTCCACT CTGAGATCTG
89551 CATGTAGCTA AACTTATCAG GTGAGTGCTT TCCCATCTTT GATCATTGAT

FIGURE 3A-28

89601 ACTGCTTGGA ATATACCGGA AAAAGAGCAG CAAGCAGAAA ATCTCCCATT
89651 TCCACAAGCT GCTGACTAAC TCAGAATTGC TAGATTTTGT GAAGCAAATG
89701 AATGCTATAA AAGAAGTCAG AAAGATCAGG GAAGCTGTCC CTAGGACTTG
89751 GTCAGGCCAA ACCTTGAAAT ATCAAGTGAT GTTACAGAGG TACAATTATG
89801 AGAATATATA TAACTCAAGA CTTACATATG TGATAAATAG TGCATTGCTC
89851 TTTGCCGTCT CCAAAGGATT TTCTTTTTTT TTTTTTTTTG AGACGGAGTC
89901 TCACTGTGTC GCCCAGGCTG GAGTGCAGTG GCGCGATCTC CGCTCACTGC
89951 AAGCTCTGCC TCCCGGGTTC ACGCCATTCT CCTGCCTCAG CCTCCCGAGT
90001 AGCTGGGACT ACAGGCACCC ACCACCACGC CCAGCTAATT TTTTGTATTT
90051 TTAGTAGAGA CGGGGTTTCA CTGTGTTAGC CAGGATGGTC TCGATCTCCT
90101 GACCTCGTGA TCCACCGCGC TCGGCCTCCC AAAGTGCTGG GATTACAGGC
90151 GTGAGCCACC ACGCCTGGCC AGGATTTTAT TTTTAATTCT CACAGCAATT
90201 CTGCAGAGAG AGGTAGTGAG AGGTTTAATG CTTTGTTCAA CATAATTTGC
90251 TGTTAAATAG CCATTCATTG GCAGAAAATC TGAACTGTTG TGTTTTCCTT
90301 CCTGTGTCAT TCATGGTTTC AGTCCTGAAG AGGAGCCCAC TAGAGCCCAA
90351 CAGGAGAGGA GAGTGGGAGA ATCCCTCACC CAGAAGTTCA CAGTGGTATC
90401 ATTTAGTGAC ACTCAGGATG TCTCCAGTTA TTGTTAGAAT TTAAAGTTAG
90451 GTTCATCCCT GTGAGGTCCA AGAAAATATA AAAATAAAAT AAGGGTCTAC
90501 TAGTATTAAA CATACTCTGT AATCACTTTT GAAAGGAAAG GAGTTAGTGG
90551 AAAAAATGGA AGAACCATAG CGAAACTAAA ATAAATATAT GTAGATATAT
90601 TGCTGGACGT GGTGGCTCAC ACCTGTAATC CCAACACTAT GGGAAGCTGA
90651 GGCAGCCAGA TCACTTGAGG TCAGGAGTTC AAGACCAGCC TGGTCAACAT
90701 GGTGAAACCC CGTCTCTACT AAAAATACAA ACATTAGGCC AGGCTCAGTG
90751 GCTCACACCT GTAATCCCAG CAGTTTGGGA GGCTGAGGTG GGCGGATCAC
90801 CTGAGGTCAG GAGTTCGAGA CCAGCCTGGC CAACATGCTG AAACCCCATC
90851 TCTACTAAAA ATGCAAAATT TAGCTGGGCA TGGTGGCACA TGCCTGTAGT
90901 CCCAGCTACA GGGAGGTTGA GCCAGGAGAA TCGCTTGAAC CCAGGAGGTG
90951 GAGGTTGCAG TGAGCCATGA TTGTGGCACT ACACGCCCGC CTGGGTGACA
91001 CAGCGAGACT CCATCTCAAA AAAAAAAAAA TTACATATAT ATACACATAC
91051 ACACACACAC AAACATTAGC CGGGCATGGT GTTGTGCACC AGTAATCCCA
91101 GCTACTCTGG AGGCTGAGGC AGGAGAATCG CTTGAACCCA GGAGGCAGAG
91151 GTTGCAGTGA GCCGAGATTG CACCACTGCA CTGCAGCTTG GGTGACAGAG
91201 CGAGACTCTG TCTCAAAAAA TATAGATAGA TAGACAATGT TAGATAACTG
91251 CATAATTATT ATATGTGTGT ATTAATATAC GAAGCAATCA CTTTCAGAAG
91301 GAATAGTGTG TTAAAAAAAG GTAATGAAAG ATTTTAAAAC AAAACACTTC
91351 ATGAGACAAG AAGTTAGAAC AATTACGGCA AACTAAAAGA AAAAGCTAGG
91401 AATGAGATCG AATACAGCCA AGTATTTCCT GCAGTTTTAA AACCTCTACT
91451 CCCCATTTTG GGTTTCTGGC CACAGATTAC GTAATATTTT TCGTTACTTG
91501 AACTGGAATT ACAAAGATTG ATACAGAAGA TGGTCCGATA AGTCAATTGG
91551 GTCCTGCTCC TTGTATGTCT AGGTCCAAAC CAAAATGAGT CAATATTTGG
91601 ACAAGATATC AGCCATCCAG GGCTTATAGG CAGGTAAAGG AGATGGCCCA
91651 TTATTACAGG GATTTCAAAC CAGGCTTTGT ATTCTCTTAC CCTGGCACTG
91701 CCAATTATAT TTATTTATTG GAAAATGATA ACCTTAGAGT TAAGCTATAT
91751 GCTTATAAAA GAGGCACTGC TTATATGGGT TCTATCATGT CCAGGTTTAC
91801 ATTGCCCGTT AGAAAACAGG ACACCTGGCT GGGTGCAGCA ACTCATGCCT
91851 GTAATCCCAG CACTTTGGGA GGCCAAGCGA GTGAGGATCG CTTGAGCCCA
91901 GGAGGTCAAG GCAGCAGTGA GCTGTGTTCA CACCAGTGCA CTAGACACCA
91951 TCTCAAAAAA AAAAAAAAGT GTTGGGGGGA GAGAGAGAAA GAGAGAGAGA
92001 GAGAGAAGAG GAGGGGAGGG GAGGGGATAC CTGATCAGAC TCCTCTGAAG
92051 AGGGAATTGA AAAGTTTGTC ACAAGCCCTG AGTTATGCTG ATATAACAGA
92101 GAATTGTTAG ATCAGAGAAT CCAAAGTAAC CTACTGCGCT TAGCCCTTCA
92151 GTCTTTGTCC TAGCTATAGG CCATAAAGTT GAATAGTGCC GGGAATTGTT
92201 CTTGACTTAA GAATATAATG GTCAAAAAGG ACAGGCAAAG TTGTTTCCCT
92251 TCTGGAACTT ACACTTTAAT GGGGGAGATA GACAATAAGC AAGTAAAAGT
92301 AATTGAACAA GGCAATTGCA AATACCACCC TCGGTGAGCT CTTGAAACAC
92351 AAATTATTTC ACCTGCATTC CACAGATACA CAGGTGAATG TTTGCCTTGA
92401 TAAATGCATA AAAGTGACTG AACTTTTGAG GTCCACTGGG CTTTTGTTTG
92451 ATATTTACTG CTAGTGAATT TTCCAGCCTG CAAATCTCTT AGAACTTCTA
92501 AATACATTTT TTTTTCTTTT AGGTTGCAGA GAACACATCT TAGAAGATGA
92551 AAAACCTGAA TCTATCAGTG ACACTACTGA CTTGGCTCTA CCACCTGAAA
92601 TGCCGATTTT GATTGATTTC CATGCTCTGA AAGACATCCT TGGGCCCCCG
92651 ATGTATGAAA TGGAGGTGAT TCATTCTTTT TATTTCTTTT TGCTCCAGTC
92701 AATGAAAGGA ACACTTTATT GAGGCCCCAG GGCCGTAGGG CCTGGGCAGG
92751 AGGCTGCCCT TTGGGGAAGG AATAGCCTTA TTCGACCTTC TTTTTGGGAC

FIGURE 3A-29

92801 GCAGGTTGTT GGTGTGGCCG CACTTCTTGC AGCAGTTGAC TGCATGGGGG
92851 CGCAGGCGAG CACAGCTCTT GTGGCACATC ATCTTCTTGC AGTTGTATTT
92901 CTGGGCAAGG TGGCAGAGGG AAGGCTCCGT AATGCCACCT CACAGGCACA
92951 GCATCAGGCG CAGGGTGGAC TCTTTCTGGA TGTTGTAGTC TAAGAGTGTG
93001 TGGCCATCCT TCAGCTGTTT GCCCTCAAAT ATCAGACACT GCTGGTCAGG
93051 TAAGATGCCC TACCTGTCTT GAATTTTGGC TTTGACATTC TCAGTGGCAT
93101 CACTGGGCTC GACCTCAAGG GTGATGGTCT GGCCTGTGAG GGTCTTCACA
93151 AAGATCCACA TCTCAGCGTC TGCAGCTTGG CCAGTCTCAC TCCATTCTCA
93201 TTTTTTTGTT GGTACTCACT GGTGTACTCA GGTGGTTGCT TAACAGAGAA
93251 GTAAAATTGG ATGTTTCCAG AGGCTGAATT TTGCCTTAAG ATGGAAACTT
93301 TATTTCTATA TGGTATTGTG TTTTAGTGCT TATTGTGATA ATATGACTTG
93351 CCAGGAGCCA GAGATCCCAG CCATATCCTC TTTTAGAACC CCAGTCTCAT
93401 TTTATTCTCT ACCATTCAGT TCCATTTTAA GGACAATGCC TCTGACTCTT
93451 CTTCTTAGAA AAATTACATA TTCTTATGTG TACTTTAAGG AGGGATTTCT
93501 TTGTGCTATC AAGGGCTTGG GGGAAGAGGC GGGGAATCAA CCTGATACAG
93551 GTCTGAAAAC ATGAGCATAG CTTAGCTTCA GACTGTGCTA GTGCAGACCC
93601 AGATGACATC TTTCAGGAAC CTATTGTTCC ATTGTTAATA GTTCCTTTAG
93651 GGTTAAACCC ACATGCAGGT CTAGCCCTAT TTTCATCTTT CTCTCCTAAC
93701 TGTACCTCAC AGCAGAAGGC CTGGGTGCCA AGACCGAGTT GAAGCAGCTG
93751 ATGGAAATAG ATGTTAGACT ATAACTGCTA AGGGCATTGT GAAATAATTT
93801 ATAGGTGCTT AGATGAGCTT TCATAGGTTG GTTACTATAA AAATGTTTGT
93851 ATTATACTAC TGAATTTAGC TTTATCATCA CCTCCTTATC AGTTTAAGGA
93901 AAAAATATTT TCAGAAAATA AATCTGATAA ACTATGTAGA AGATAATCTC
93951 TCCATCTAAC ATTTGAAATC ATTACCAGTA GATATGGTTT TCCTCAAGTT
94001 CTTACAACTG AGCAGATGAG AAATAGCCCC CAAGCCTGTC TTGTTTATCC
94051 ATTTAAACTC TAAACTGGTC ATTAAAGCTA ATGAGCCTCT CTACAGAGCT
94101 CTCAGTTACA AGAATAGAAC TTGTTTACTC TTGACAGTAA ATCTGGACTT
94151 GAACAATAGA ATCAGAAGCA TTGTTTTGAT TATTTGAATT CTTAAGATAT
94201 CATGGATTTG AATTTTGAAG TGTTGAAAGA ACTTGAGCAA AACATTGTTG
94251 ATTGAGAAAG TGAACAAAAC CTGCTTTCTC GTTCTGGGAG GATCCAGTGA
94301 CATTGTGAGT GAAGACGCAA ACAGGTTTTG ACTCCTGCAT GGCCGATGAC
94351 CTTTTTCTGT AGGCTTACCA GAAAAGTACA TTCCAACAGT TCTTTGAGGA
94401 TTTAAACTAG AGCAGCAAAT AAAGACAAAA GATTAATGCA TGTCTCTGTT
94451 GCATATACCC CTCTCTCCCA GCCATTTCTG CTGATGTTAA GTTTGGAAGC
94501 ATTGCTGACA TTCCTGGAGC ATTAGCAAAG AAAGAGCCAA GAGAACAGAA
94551 ATGAGAAATT TTATAAACAC TGCTTACCAG TTATCCTTGT TAGCATGGGA
94601 GAACCTTATT TTCCTTGTAG CATGTGAGCT TTAACATAGT AACACTTTTA
94651 CCAACATGAG TCTGCAGAAA GACTCCAGTA GCCATTTTGT CTTTTATAGA
94701 TAGCATCTTA GAATGGAAGA TGTGGTGTGT CACATGCGTG CGTGCGGAGA
94751 GACCACCAAA CAGGCTTTGT GTGAGCAACA AGGCTGTTAT TTCACCTGGG
94801 TACAGGTGAG CTGAGTCCGA AAAGAGAGTC AGCAAAGGGA GATAGGGGTG
94851 GGGCCGTTTC ATAGGATTTG GGTGGGTAGT GGAAAATTAC AGTCAAAGGG
94901 GGTTGTTCTC TTGCTGGCAG GGGCGGGGGT CACAAGGTGC TCAGTTGGGG
94951 AGCTTCTGAG CCAGGAGAAG GAATTTCACT AGGTTAATCG CTCAGTTAAG
95001 GTGGGACAGA AACAAATCAC AATGGTGGAA TGTCATCAGT TAAGGCAGGA
95051 ACCAACCATT TTCACTTCTT TTGTGATTCT TCACTTGCTT CAGGCCATCT
95101 GGATGTATAC ATGCAGGTCA CAGGGGATAT GATGGCTTAG CTTGGGCTCA
95151 GAGGCCTGAC ATCGTGTTTT GAGTGTTGGG AACATTGTGT TCATTTTTTT
95201 CATACTTGAA AGTGAGAACT CACCCTGTAG CCGGGTGTCT CTACCTGTAG
95251 TGGTCTGATG ACCACCAGCC CCAAATTACT TAACCACACA GTCTACCTCT
95301 GCTTTTGCAT CTATAAAATT AAGATTTATG GAACATTTCT TTCTTGTCCG
95351 TGAGGGCTGT CACTGTGCTA GGAGTGTAAT TCCATTTTAC ATACAAGGGA
95401 AAAAGTTTGA AGAGATTAAA TGAATTGTAC AAATTCACGT AAGTGGCAGT
95451 TGGTAGAGTT AGGATTCAGA CTCAGATCAG CTTATTCCAA GTCCATTATT
95501 CTTTCTACCT TTCTACAGTA CCCTGTCAGG CCAAAATAAT TCCTGCCCTT
95551 GTCTGCTAGA AGAGAGTGGC AGTGATGTAT GAGAGTTTTT TAAAAAGGCA
95601 TCTGCTCTAC ATCAGATTCT CATTCATATT CTTACCAACT CTGTTGCTCT
95651 GTTTTGGAAT GGGAGAGGCT GGGCTCAACT TGTTGACCAC TCCCATTTTT
95701 GTATCTCTTG GCTATCAGGC ACTGTGTAAG GCCCTCCACA GTGATCATTT
95751 AATCCTCAGT CATGGTTGTC TTTCCAATAA CAGTTGAGGA AACAGGCTTA
95801 GAGTATTTAA ATAACTTGAG AGAAGACACA ACTTATGCCA GAAATGAGAT
95851 TTGGTTCTAG ACCTGACCAA CTCCAAACCT AGTGCTGTTT ATTACTCTAG
95901 AAAAACATCA CAGGCAACCT GAGCAGGGCC TCTGTTCATT GCAGAGAGCT
95951 CACAGGTGGA CCTGAGCAGG GCGTCTGTTC TTTGCACCTC ACAAGTGGCC

FIGURE 3A-30

96001 AGTCTTATTT CTCTACTTCT TTGTGCTTTC CTAGGCAAAG AATCTGAAGA
96051 GAGAGGTTAT ACTAGGAATA CTGGAATACA TGTTGAGGTG TTCCCAAGAT
96101 GTTATAAGAT ACCTTTCATT TGTTTGTTTT TACTTTTTGA GATGAGGTCT
96151 CACTCTGTCA CCTAGGCTGG ATTGCAGTGG CATGATCATA GCTCACTGCA
96201 ACCTCCACCT CCTGGGCTCC CACTTCAGCC TCCTGAGTAG CTGGGACCAC
96251 AGGCGTGTGC TACCATACCC AGCTAATTTT CTCTGTATTT TTTTGTAGAG
96301 ATGGGGTTTC ACCATGTTGT CCCAGACTGG TCTCAAACTT CCTGAGCTCA
96351 AGCCATCCAC CTGCCTCAGC CTTCCCAAAG TGCTGGAATT ATAGGCATGA
96401 GCCACCAAAC CCAGCCGATA CCTTTTTTTT GTCTAAATGC CTGTATTCTC
96451 CCTTAGGGTA AATTACAGTC TAGGGTCTGT GGTTTCTTCT AGAAAGAGTT
96501 TGATTCATTT AATAAATACC TATTAAGGAC CTAACATGTG CTTCTGGCAA
96551 CACAGTAGTA AACAAGCAAG GTATGATGTC TGCCTTCATG GATCCCACTT
96601 TAATGCAGGA AAACAATAGA CAAGTAAACA AATAATCACA AATTGAAGTT
96651 GATGCTATAG AGAAAACAAA CAGGGTGGTA CTGAGATAGA CAGTAACTAC
96701 TCTAGCTATA TCTGAGGTCT GTTTTAGAGG TAGAAGTAGA CATGCTGATG
96751 GGAAACATTT GGGGAATGAA GGAAACAGTT ATCAAAAGGG ACTTACAGGT
96801 TTCTGGCCAG AGTGACAGGG CATGTGTAGT AGTGCTGTTT ACTGAGATGG
96851 GGAAGACTTG GGGAGGGAGA TGAGGAGAGA GTGTTGCAAA GAAAACTGAG
96901 AGCTCTTTTG AACACATTAC AGTTGAAATA TCCAGGCTGG GCGCGGTGGC
96951 TCATGCCTGT AATCCCAGCA CTTTGGGAGG CTGAGGCAGG TGGATTGCTT
97001 GAGTCTGGGA GTTCAAGACC AGCCTGGGCG ACACGGCAAA ATCCCTTCTC
97051 TACAAAAAAT ACAAAAATTA GCTGGGTGTG GTGGCTTATG CCTGTAGTCA
97101 CAACTACTTG GGAGGCTGAG GTGGGAGGAT CACTTGAGCC TGGGAGACGG
97151 AGGTTGCAAT GAGCCAAGAT CACGCCACTG CATTCCAGCC TGGGTGACAG
97201 AACAAGACCC TGTCTCAAAA AAATAAAATA AAAGTTAGAA ATATCTGTGA
97251 GGCATAGAAG TAGAGACATT TGGACATTCA GATCTATTGC TCAGAGGAAA
97301 TACCCAAGAT GGAGATTTTA GAATTATTAG AAAATAGAGG ATATTTAGAG
97351 CCCCAGATAT TGAGGCTTTC ACATCACCTA AGAAAAAAGG ATACATTTTT
97401 AAAAAGCAGG TAGTCTAGAA GCAAGCCCTG AAGAACAGCA TTATTTAGGG
97451 ATCATATAGA GAGAAGAGGA GCCAACAAAG AAGTCGGGAA AAACAGAAAG
97501 GGACTGGGAA GGAACAAGCC TTCAGGGAAG AGGAAAACCA GGATGTTGTG
97551 CTGCCATAGA GACAGAAGAG GAGAGTATTT CAAGAAAGAG GGGACATCAA
97601 AATGTGTTTA CTGTTTGAGA GATCAAAAGA AGATCAAGGT CAGAACAAAT
97651 GTGTATTGGA TTTGATGGCA TGAAGGTTGT TGGTGACCTT GAAAGAGATT
97701 TCACAAGGAA GGAGTGGTGG GGATGGTAGA AATTGGAGTA TGTTGAAGAG
97751 AGAATGGGAG GCGAGGAAGT AGAATTAGTG TGTAGGCAGC TCTTTAGAAG
97801 TTTGGCTGTA AACAATTGCA GAGAAATGAG GCAGCTAGAA GAGAATATGG
97851 ATGTCAAAGG GAGAATGTTT TCAAAATAGT AGCTGCTGCT GAGAGTAATC
97901 CAGTAGAGAG CACAGACTGA TGTTGCAGGA CAGAGCAGTG GTACGATAGA
97951 AACAAAGTCT CCAGGAAAGT GAGAGGGGGT GGGACCCAAA GCACCAGTGA
98001 GGAAATGGCT TTTGTTGGGA GAAGGATAC CTTTTGCAGG ATATTATGTA
98051 GAAAGGGACA AGAATATTGA GTTATTTATA AGGAAAAGAT TATAATGATG
98101 GGGCTAACGT GTGTGAGCTG CACAAGAGAG GAGTGAAGTT AGGGCAGAGC
98151 TGCTGTATGA TGGGAATGTG CTGGAGTTCA TGGCTTGAGT ACAGGCGAGC
98201 TAGAAGGATA AGAAATGATG GTCAGGGGTT TCAGAGGTAG CATGGTTTCT
98251 GTTGGTGATA AGTACCTGGA AGAGGGTGGC TGAGTTCAGG AGGCATTTAA
98301 AGAACTGAGA AGCCAGGTTC TGGGAGAGCA TCATGCCTTC ACTGAAGACA
98351 CCCAGGGTGA TAGCAGGGGC TGGGGCAGAA AGGAAGGAGC AGAGTTTAGA
98401 ATCTTCCTGA ATGTCAGAGA CAGTGAAGAG AGAGTCAGGA TGGTAAAGCC
98451 AGCTGCCATA AGCAGGGGCT CAGAAGGGTA GAAGAATAAG GCCTGAAAGT
98501 TGCAAGGCAG CCTCTTACTG ACTAAATTTT AAACTTAGTC TCTTTGAGCT
98551 TGATGTCTTC CTCTGATAAA TGGTGGTAAG CATGTGCACG TTATCACAGA
98601 GTTCAAATTT GGTGAGTCAG TGTACCCACT GCATTGCCCA GTAATACTAA
98651 AAAAGAAAAA ACAAATACTA ATTTCTGCAA CTACCATACT CCCTAAAAAC
98701 AGAGACCTAC CCCCAATCAC CAAAAAATCC CCATTGTTTT TCTAATCCAA
98751 ATTTTGTACA TATTTAATAA CCTTATACCA CCACTTACTA TTTTTTTACT
98801 TTCATCGAAG ATGAATCTAC AAAAATATAT TAATGTCAAA AAATATTACT
98851 GACCTAGCAA ACTGGCAGTT GGGAAGTAAG GTAAGAAGGC ACACTTTTAT
98901 TAATTAATAA TATCTTTTGT ATTCCCTAAA CAGATTGAAA AATGATGGAT
98951 TAGTTCATTC TTGCATTCCT ATAAAGAAAT ACCTGAAACC AGGCACAGTG
99001 GCTCACGCCT GTAAATCCCA GCGCTTTGGG AGGCCAAGGT GGGCGGATCG
99051 CTTGAGTTCG AGACCAACCT GGGCAGCAAA GTGAGACCTG GTCTCTACAA
99101 AAAATACAAA ATATTACCCG GAAGGCTGAG GTGGGATCCA CCTGAGCCCA
99151 GAAGGTTGAG GCTGCAGTGA GCTGTGATCA CACCATTGCA CTCTAGCCTA

FIGURE 3A-31

99201 AGTGACAGAG TGAAAACTCT GTCTCAAAAA AAACAAAGAA CCACCTGAGA
99251 CTGGGTAATT TATAAAGAAA AGAGGTTTAA TTGGCTCACG GTTCTGAAGG
99301 TTCTAAAGGA AGCATAGCTC CAGCATTAGG CCAGGTGCAT TGGCTCACAC
99351 CTGTAATCCC AGCACTTTGG GAGGCCAAGG GCAGGCGGAT CATGAGGTCA
99401 GGATTTCGAG ACCAGCCTGG CCAATATGGT GAAACCCTGT CTCTACTAAA
99451 AATACAAAAT TAGCTGGGCG TGGTGGCGCA CACCTGTAGT CTCAGCTACT
99501 CGAGAGGCCG AGGCAGAAGA ATCACTTGAA CCCAGGAGGC GGAGGTTGCA
99551 ATGAGCTGAG ATCGTGCCAC TGCACTCCAG CTTGGGACAC AGAGTGAGAC
99601 TCCATCTCAA AAATAAATAA ATAAATAAAT AAATAAATAG CTCCAGCATC
99651 AGCTTCTGGG GAGGCCTCAG GAAACTTACA GCCTTGGCAG AAAGTGAAGG
99701 GGGAGCCGGC ATGTCATGTG GCCAGAGCAG GAGCAAGAGT GCAGGAGGGG
99751 AGGTGGCCAC ATGCTTTTAA ACAACCCACC TCCCACAAGA ACTCACTCAC
99801 TATTGCGAGG ACGACAGTAC CAAGGGGATG GGGCTAAACC ATTCATGAGA
99851 AATTTCCCTC CGTGATCCAG TCACCTCCCA CCAGGCCCCA CCTCCAGCAC
99901 TGAGGATTAT AGTTCAACAT GAGATTTGGT GGAGACACAG ATCCAAACCA
99951 TATCAAATGG GTTCTAGGAA CTTAGCCTAG ATTTCAGATT TAGGAACAGT
100001 ATCATAGGTC ACCTTTTCAA AATACATAAA GTTTCCTACA GAAACAATAT
100051 CAATTAAGTG CATGTTTTAA AAATAAAAAT AAAGGTTACT ACAAAAAAAG
100101 TGGGGAGGAG CAGGAGTGGG TGCAGGTGTC CCCAGGAAGC CTAGGCATAG
100151 CTCACACTGC ATGTGCTATC ACGGCGAGAC TCAGAACTGC CCCGAATCCG
100201 AGGAGGGGCC ATGCGAGTAG GTGGGCCTAG GCACCTCCTC AGTCACTGGC
100251 TGTGCCCTTT CACTCTGTCA CTGGGAGACA GAATCCTGAG TTTTCTGCTT
100301 CAGGGAGCCT GCATGGAAAG AGTAGGTCAC TGCCGGAAAT CAGGCTAGTT
100351 TTAGCAAAAG GAACGGACAT TAGGCACCTC CAAAGGGACA AAGGACCAAT
100401 ATACCTGGTT GGGGACAGGA TTCTGTCATT TGATTATTCC TGACTCATGT
100451 TTTCATGAGG TAGTCCCCCA CCTCATATAA AAGCCTCAGT GTTGGCTTCT
100501 GACCATGGTG TATGAAAAGC CCTTGTCTAA AGGTTACTGC CCTGAGAAAA
100551 TAATAAAGGA AGAAGAGGAT AGACATGAAG ACACTTTAAA GCCTCCTGAA
100601 TAGAATGCAT CCAGAAGCGA ATTCCAGGAG ATTCTGTCAT CATGCTTGCC
100651 TTTCAAGCAA ACAAAATTAG CTGCTAGAAC TGAGAAAGAG TGTAAACACC
100701 AACTAAATGC CTCAAAGAAT CATGGTAGTA AATTACTTCT CCATGTTGCT
100751 CCATATAAAC CTGCTGTGCC ACCTGTTGAA GGCAGCACTG ATGCTGCATG
100801 TTCAGTCTGG TCCAAGGCCC CAACAGGAAT CCGTTGTGCC AAGAAAAGGC
100851 CCTACTGGAA GGATTGGAGA GCAGCTGGTT CTCAGCAATG CAAGCATCAG
100901 GCCAGGCTGG GGCTGCTTAA TGCTGCTTAA GAGATGACAG TGGTGGACCC
100951 CAACACCTCT CCAAGGGATG TAGAATCTGC TTTTCCCATT TCTGAATGCT
101001 ACTGAAACAA ATCTACAACT AGAAAAATCA AATATTCATG AATTCAAGAC
101051 TTGGGATCTC AGTACTAAGA CTTTAAAGAA GTTGCCAGAT GGATCGCTTC
101101 TGTGGTGACA GCCCTGGCAG GAGCATTCAA GTGCTCTATG AGCTACAAAA
101151 GAAACCAGTT GATGGTGTGA ACACCACTAC AGAGCAACCT GCACACCACA
101201 GCAATTTGAC AGCTCAGGTT CTGTGTCTCA TGTGGCACCG TGCTTGTCCT
101251 TGGAAAGAAG GCCTACAAAA TTCTTCATAT CTCCATTCCT TGACATCTGC
101301 TGGCAAACTC CCACTCATAT TTTAAGACTC AGCCTCTCCT GTGACACCTG
101351 TGTCTTCTCT CCAAACAGGG AGGGACGCTT GCCTCTTCAG AGCTCCCCAC
101401 ACTGGAGTAT AACTGCTCCT GTGTCTGATG CCCTTAGTCT CAGTGCCAGG
101451 AGGTATTCAT GCTTATGTCC CCATGGCCTG TAACAGAGCC TGCATCAGGA
101501 TGCTTGGTAA AGGACTGTTG AATGAATGTC AAATATGGGT CCCTCTGATG
101551 GGTCTATACG TGTTGATCTA GGATTGGAAG GGTCACAAAG AGTTGTGCAT
101601 GCTTACAATT TCAATCAAAT ATCACTATTT TTAGTTAAGA GGGAAGAGTA
101651 GTGTGAAATT GGCAATAATT AGATACTCCA AATGTTCTTT AAAAACTAAT
101701 AGCATTGATG TATTAAGAAT GCAATCAGCC GGGCACAGCA GCTCACACCT
101751 GTAATCCCAG CACTTTGGGA GGCTGAGGCA GGTGGATCAT GAGGTCAGGA
101801 GTTCGAGACC AGCCTGGCCA AGATTGTGAA ACCCCCGTCT CTACTAAAAA
101851 TACAAAAATT AGCCGGGCAT GGTGACGCAC ACCTGTAGTC CCAGCTACTT
101901 GGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCAGGAGGTG GAGGTTGCAG
101951 TGAGCCCAGA TCGTGCCATT GCACTCCAGC CTGGGTGACG AGCGAAACTC
102001 AGTCTAAAAA AAAAAAGAAT GCAATCATAC ATTAGAAGAC ACATTCTGTT
102051 TTAGATTTTT ACTTAAATAT TTTAAATACT TCCTTAATCT GCATATTTAC
102101 CTTATTGATA GATTTCAGAA GAAATTGATC ATTTCATGGA ACAAGATTTA
102151 TTAGACACAT AAGGAAAGTG AATCATAACA ACTGTACAGG TGGGAAATTG
102201 AACAACAAAA ATGACCCTGA GATACCCACA TTCTACTTTG GCATATAGTG
102251 GGAAAAACAT TCTAGACTTC AAGTCTAGGC CTATCTTGGC TAATGTAACC
102301 GATGACTTCA CAAACCATTT ATGGGACTAG AAGCTGAAAG GAAAGTACTG
102351 GTGGATAAAC ATCATATTGA AATTATGTTG AGTCACTTAT TTGCTATAAA

FIGURE 3A-32

102401 ACACAAATTG TTTTGTGTAA AGGGGTTAAG ATGGCTGGAA AACTGTCTCC
102451 ACTCAAGAGC AAGAAAGCAG CATGTGTCTT ACCCTGTACC TTCATTTTTA
102501 CTTGTACTTC ATAATTTCTG AGGGAGAAAT ACGTGGAAAC CAGATGCTTG
102551 ATATAGTTTC AGAACACGTC CTTAAAGAAT ATGACTCCAA GTCTAAGAAT
102601 TGTAGGTCCT TTGCTTCTTA GATAACTACT GTTAGCCTTG ATCACAGAGA
102651 TTCCAGGTTT AATAACTTCA GTTCTCCCCA CTGTGTATAT AGATGTTAAG
102701 TTACACAGAT TTGGCATTAT TCCCATTTTC AGGTTAATAT CAGAACACTT
102751 GTTATCAAGT CAGGATAGTA ATTGTGAGCC TAGATGCTCT AGGTTTGGCC
102801 ATACGTGGTT ATCTACACCA CCAACTGTTC CAATTAACAA TTTACCAGTT
102851 GCTTCTACCC AAAGTACCAA GACTCCAGCA AATGGGGAAT ATTGGAAACT
102901 GGCTTGGCTT CTTGAAGCAA CATGGTAATC AATAAGAATC TTGGCTGGGC
102951 ATGGTGGCTC ATGCCTGCAG TCCCAGCACT TTAGGAGGCC AAGATGGAAA
103001 GATGGGAAGA TCGCTCAAGC CCAGGAGTTC AAGACCAGCC TGGGCGACAT
103051 CGTGAAACCC CATCTCTACA AAAAAATACA AAAATTAGCT GGGTATGGTC
103101 GTGGGTGCCT GTAGTCCCAG CTGCTGGGGA GCTGAGGTGG GAGATCACCT
103151 GAGCCCAGGA GGCAGTTGCA GTGAGCCAAG ATTGCACCAC TGCACTCCAG
103201 CCTGGGTGAC AGAGTGAGAC TCTGTCTCAA AACAAACAAA ACAACAATCT
103251 GGCTGGGCGC GGTCGCTAAT GTCTGTAATC CCAACACTTT GGGAGGCTGA
103301 GGAGGCAGAT CACTTGAGGT CAGGAATTCG AGACCAGCCT GGCCAACATG
103351 GTGAAACCCG TCTCTATTAA AAATACAAAA ATTAGCCGGG CATGGTGGCA
103401 CACACCTGTA ATCCCAGCTA CTTGGGAGGC TGAGGCAAGA GAATTGCTTG
103451 AACCAGGAGG CAGAGGTTGC AGTGAGCTGA GATCATGCCT CTGCACTCCA
103501 GCCTGAGCTA CAGAGCGAGA CTCTGTCTCA AAAAAACAAA AAACAAAAAC
103551 AAGAAGAATC TTACTACTGC TTCTTCGGGG ATACTTTTGG TATTATTTTG
103601 ACAAATGAAT TGTGAGGATT CAAATATAAG AAAGGGATTA TTCTTGGTAG
103651 AGTTAACAAA ATTGTACCAA ATGACTTTTT GTGTTAAACA CGATTCATTC
103701 ACCCAACCCT AGAAAGGAGC CTGAATGAAG TCTAATTTGG GTGACAGATT
103751 CCCACACAAA TTAGATGTAT GTCATTCAGG TATAGAGAAT TGATTTTATA
103801 TTAGAAAAAA CAAACCTTGT AAACAGTTTT ATAAATAACT GTTTCATGAT
103851 TTTCCTTAAG TAGTACTGAT CTCTTACATA TAGATCGTTT GTGTCTTTCG
103901 CCTCAAGTTA GTATAGAACA GGGCAAGTGG CAAAGCTCGA GGAAAGTGTG
103951 ACCTGAGGTA CATGCTGTCA GCTTGATGCT GGAGTTTGGC CTCTCAAATC
104001 TCTAACCTGT TAAATGAAGT TAATTAGGAT TAATTTTTTT TAATGTATGT
104051 TTACTACTGA AAATAAGTGC TCGGCCAGAC GCAGAGGCTC ACGCCTGTAA
104101 TCCCAGCACT TTGGGAGGCC GAGGCTGGCA GATCACCTGA AGTCAGGGAG
104151 TTTGAGACCA GCCTGGCCAA CATGGCGAAA CACTGTCTCT ATTAAAAATA
104201 CAAAAATTAG CTGGGTGTGG TGATACATGC CTGTAATCCC AGCTACTCGG
104251 AGCCTGAGGC AGGAGAACTG CTTGAACCCA GGAGGCGGAG GTTGCATTGA
104301 GCCAAGATTG TGCCATTGCA CTCCAGCCCA GGCGACAGAG TGAGACTCAT
104351 GTCTCAAAAA AAAAAAAAAA AAAAAGAGGA AAAGAAGTGC CCAATAGCTT
104401 CAATGGATGC CACATAATTT TGGAATAATT TTTACAATCA GGAATTTCAT
104451 TGTCCAAGCC CCTTAGAAAA AGAAGCAACC CAGCCCCATA CCCAGAAAGT
104501 CAAGCTGTAT AGTGCTGTTC CTTAGTGAGG ACGGTCAACT CTCAGTAGAA
104551 AAATCTCCTG TTTGGATTAG TGCTTAGTTG ACCTATTGTG TTCAGTTCCT
104601 CTAACATGAG TAACTTCTAT TGGATAGGAA ATTTTGAAGC TCAAAGGGTG
104651 TAATGAGAGT TAACATTACT GATTTTCCAC TGTTACTTTT TAGTGTTTTC
104701 ATAACTTGGA TGTGTTAACC TATGGCCCAT CAACTATGCT CCTAGTCTCA
104751 GGTGACAACA TGTTCAATTT AAGATGGCAG GCAGTACAGT GGACCTCTCT
104801 CATCCCATGG GAAGGAACCC AGGATGTTTA TTATGTAGTA TTGTATAGTC
104851 TCTGCAGCAG TAATAGAGAA AGTTAAAGGT AAGCGGTGGA GAAGTAAAAT
104901 CTAGAGTTTC TAATATAACC CTTCTCACTT TTCTTTTCAA AAAAAATAAG
104951 AGGGTCTCAC CATGTTGCCC ACACTGGTCT CTATCGAACT CCTGGGCTCA
105001 AGCGATCCTG TCGTCTCAGC CTCCCAAAGT GCTAGGATTA CAGGCATGAG
105051 CCACTCTGCA TGGCCAAGCT CACTCTTCTT AAAGGTCTGC TAGTAAGAGG
105101 GTTTCTACTT TTTGAAACAA ATTCATGATT ACCTAAAATG AAGCTAGGTT
105151 ATGAAGTATA TATAAATATG CAGCCCAATA GGCTGGGTGT GGTGGCTCAC
105201 ACCTGTAATC CCAGCACTTT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG
105251 TCAGGAGTTT GAGACCAGTC TGGCCAACAT GGTGAGACCA CATCTCTACA
105301 AAAAATACAA AAATTAGCGG GTGTGGTGGC CTGTGTGCGC CCATAGTACC
105351 AGCCACTTGG GAGGCAGAGG CAGGAGAATC ACTTGAAGCC AGGAGGCAGA
105401 GTTTTCAGTG AGCTGAAATT GTGTCACTGT ACTTCAAGCC TGGGCAATGG
105451 AGTGAGACTG TCTCAAAATA TATATATATT TGCAGCCCAA TAAAGATACT
105501 TAGATAAAAC TATTGGGTTT ATTCCTTGAA AACTAGGGCA TGTGTAGCTA
105551 GATCTGGCTC ATAAAAAGCA AAGTTATTTA CATATATTTT AAGGTAAAAT

FIGURE 3A-33

105601 TGCCTCTGAT AAATGTCAAA GAGGAAGTTT AGGTCTTTCT TCTGGCAGAA
105651 AGCCAGAGAG TAAGTGCTGA ATGTGACGCA GAATCATGTT AGGTAACAAG
105701 GACTTTGAGG TAAGTGGCTG AAGTCTTCTG TGGAGTCAGC CGACTCTTGC
105751 AGGATTGTGT GGTATCAGTC ACCTTTAGCA TTTGCCAACC CAACTCTGAT
105801 CATTCTTCTT CTTTCAAGGT ATCTCAGCGT TTGAGTCAGC CAGGAGTAGC
105851 AATAGGTTTG GCTTGGACTC CCTTAGGTGG AGAAATCATG TTCGTGGAGG
105901 CGAGTCGAAT GGATGGCGAG GGCCAGTTAA CTCTGACCGG CCAGCTCGGG
105951 GACGTGATGA AGGAGTCCGC CCACCTCGCT ATCAGCTGGC TCCGCAGCAA
106001 CGCAAAGAAG TACCAGCTGA CCAATGGTAG GAGCCTGCAC CCGGCCAGGC
106051 AGGCGTGACC CAGGAGGCGG TACCTTCCAT GGCGGAGACT GGCATGAGCT
106101 CGAGACTGCC AGTTACACAT CTAGCAAAGT ACACACCGTT TTGAACCCCT
106151 GTGGAAATCC TAGTTCCCAT TTCAGGACTA TTTGACTAGT GCCTGAACTA
106201 GAAACTAATT CAAAAGGTTT ATTTTGTTTT AATACGACTT AGAGTAGAAT
106251 GGAACTGTTC TTCCACACCC TCACCCAAAT TGTACTGTCC ACCAATATTT
106301 TGAAGAATTC ATTTACCCAA AACATTCATT TTTGTTTGTG ACTTTTTTTT
106351 TAGGAGAAAA AGAAAACAGG TTTAATTTTT CTACATTAAA GTCCCTTTTT
106401 CCTTTTTAAA GCTTTTGGAA GTTTTGATCT TCTTGACAAC ACAGACATCC
106451 ATCTGCACTT CCCAGCTGGA GCTGTCACAA AAGATGGACC ATCTGCTGGA
106501 GTTACCATAG TAACCTGTCT CGCCTCACTT TTTAGTGGGC GGCTGGTACG
106551 TTCAGATGTA GCCATGACTG GAGAAATTAC ACTGAGAGGT CTTGTTCTTC
106601 CAGTAAGTAT GAAAAAACAA TTTATATGGT TATTTTTTAT TTAATTTTTG
106651 AAAATTAATA TTATTTTTAA ATACGGGTTT GCCTTCTTTC TATGAAAACC
106701 TTGGTTTTAA GTATATATTA TATTTTTATG CCTGTAACTA ATTCATATTT
106751 TAAAATTTTG ATCAAATAAA AGAAAAACTG ACAATTTTTC ACATTTTCCT
106801 TTTTTTTTTT TTTTTTTTTT TGAAATAGAC AGGTCTCACT CTGTTGCCCA
106851 GGCTGGAGTG CAGTGGTGTG ACTGTAGCTC ACTATAGCCA CCAAGTCCTG
106901 GGCTCAAGCG ATCCTCCTGT CTGTCTCCCG AATAGCTGGG ACTATAGGAG
106951 CACGCCACCA TGCTCAGCTA ATTTATTTTA TTTTGCGTAG AGACAGGGTC
107001 TCTCTGTGTT GTCCAGGCTT GTCTCAAACT CCAGGTCTCA TGCAGTCCTC
107051 TCATCTCCAC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACATT
107101 CAGCCCACGT TTCCCATTCT AAGATTTGCT AAGGGAAAAA AATATTAGTG
107151 TGGTCATCAG AAATATTGGC AGTTACATGA AAATTTGAGG CCTTGTTCTA
107201 CTTGACAAAT TGTTAAAGAT ATAGCACATG TGCAAAATGG GATAGTAGTT
107251 GTTTTTAAGC TTTAAGCCCA TTTCTTAAAT TTGAAGTTTC TTTGAGACCT
107301 CCTGTCCCCC TGCAGAAAAC TTTGCTAGTA TAGAATGGAA ACTCTAATAA
107351 AGATTAACCA TATCTAATGA CTACATTTTG AAAAGGTTCT ATACATGTGG
107401 GGTCTTGAGG CTCCAGATCC TAAACTGCTT ATAAAAATAG TGTGATAAAA
107451 TGTACAGAAC TTGAGAGTAT TTAAAGTTGT TAGTTGAGTA TTAGTCTACA
107501 ACAGACTAGA CTACAATTTT AGTCCACAAC AAGATTTTGG CAGGTTCATA
107551 GCAAGATGAG GAAAAAAAAA AAGAAATAGT CTTTTTTTCT TTTTCTATC
107601 GAGATGGAGT CCGGCTCTCT TACCCAGGTT GGAGTACAGT GGCACAATCT
107651 TGGCTCACTG CAACCTCTGC CTCCCAAGTT GAAGTGATTC TCCTGCCTCA
107701 GTCTCTCAAC TAGCTGGGAT TACAAGCATG CGCCACCACG CCCGGATAAT
107751 TTTTTCTATT TTTAGAACCT CCATAGAACA AATGGGTTTT CTACTTGGTC
107801 CCCTCTCAGA GCAAATCGTA GCCCAAGTAA AGGCTTCTGC AGCCTCAGGA
107851 GAGACAGCCA CAGCGGCCTG GGGTACACCT TCAGCTCCAG ACCATTACAA
107901 GAGGCAGGAT GGAAAGCAGC AGCACTTGAA AGAAAGGCCT GTGAAAGCTG
107951 GAGAAAACCT CCTTTGAGAA CAGAGGACAA GACGGGGCTT TGGGATTTGA
108001 AAGTGGTCAA AGAATTATTC AGGAAAAAAC TATAGTGAAA AACAATTTGT
108051 TGTTAGAACT CCAACATCTA AAAGGAGTTC TAACAAACAG GAAAATGGAA
108101 TGGAACAAAT TATCCAAGAA ATAACTGAAC ATTTCCTAGA AGTTAAGGCA
108151 TCTTGAGATC GAAAGGACCA TTACTAACCA GGAAAAACAT TTCATCCCCT
108201 TGACTTTTCA GATTACTGAG GATAAAGCGG CCTCAGCACT GACACTGGAT
108251 GTGCAGTACC TTCAAAACTA TGAGGGAAAA TGGGCCAGGC GTGGCAGCTG
108301 ACGTCTGTAA TCCCAGCACT TTGGGAGGCT AAACAGGAGG ATAGCTCAAG
108351 TCCAGGAGTT CAAGACCAGC CTGGGAAATA TATCTCTACA AAAATTGTTT
108401 TAAAAATAGT AAGGAGGCTG GGTGTGGTGG CTCACGCCTG TAACTCCAAC
108451 ACTTTGGGAG GCCAAGGTGG GCGTATCACT TGAGGTTAGG AGTTTGAGAC
108501 CAGCCTGGCC AACATGGTGA AACCCTGTCT CTACTAAAAA TACAAAAAAA
108551 TTATCCGGAT GTGGTGGCGC ATGCCTGTAA TCCCAGCTAC TCAGGAGGCT
108601 GAGGCAGGAG AATCGCTTGA ACCTGGGAGG CAGAAAGTTG CAGTGAGCCA
108651 AGATTGTGCC ACTGCAACTC TAGCTTGGGT GACAGAGTAA GACTGTCTCA
108701 AAAAAAAAAA AAATAGTAAT GAAAGCTGTG AGGGAAAATG TTTTACATCT
108751 AGTCTTGTAT ACATGGCCTT AGTATCAATC AAGTGTGAAA GTAAAATATT

FIGURE 3A-34

108801 TTCAAACATG CAAGGAATCA GTTCATCTTA CACTCTTTTG AAGAAGGTAC
108851 TTTGAAGGAG TACTTCAGCA GCATGAACAA AACCTTGAAA GAAGATGCCA
108901 GTGGGGCGGG AAGGCCTGGA GCAGCCAGCC AGTCTTAATT GGAGCAGATG
108951 CAACACATTA CCCCAAAGCA AGAATACTCC ATACTCTTCA AGTTCCTGTG
109001 GGCCAGGAAT TCAGGAGAGG CTGAGCTGGG TTCTTGTGGC CCAGGGTCTC
109051 TGGCCTTACA GTCTAGGTTC CAGCCAGGCT GCAGTCACAT GAAGGCTGAC
109101 AGGCTGGAGA AACTGCTTCC ATGGTGGTTG ACTCATGTGA CTGGCAAATT
109151 GGTCCCATCT AGTGGCAGGA GGCCCCAGTT CCTCACCTGA TGGACTTGCC
109201 CATAGGCTGC TTGAGTGACC TCAGACATTA TGACTGGCCA CCTCCAGGGC
109251 AGGTGATCAA GAGAGATTCA GGCAGCAGCT CTCGTTTTTT GTGACTCAGC
109301 CGTGGAGATC ATACAGCATC ACTCCCACCA CACTCTGTTT CTTACCGAGT
109351 CACAAAGCCT GGCCCACATT CAAGCAGGGG GACCATTGTA GACATGTTTG
109401 AAAGCCACCA TAGGAGCCTA GTTTAGGGAT ACATTTTCTT CATTAACCAG
109451 CATGGAGGTT CTGGCTTTAA ACCTGTAGAG AGGGAAGTAA CCCCAGCACA
109501 CAGCTAAGCT CTGCAGGAGC GGCGCTCATG GTCAGAATCA CGTGCTGCTT
109551 TTTCAGATCA ACCTAAAGAC TAGACGGTTG TGATTACACC TGAATGCCAA
109601 TTTACTTTGA CAGCATTTAT AAAAACAATC ATTGACAGAA GAGGAACTCA
109651 TACCTATCAA CAATTTAGAA TCCCCCTCAT CAGAGTCTTT AATATAACAC
109701 CAATTGAAAC ATTAAAAAAA GGTTACTACT TATCCTTTTT CCTGGCTTTC
109751 CTAGCTCATG CTATAACAAA ACGGAAGATG ATTTGGATGT TTTAAAATAG
109801 TAGTGGTTAA ATTCAGTGAA AGAAAGCTGG GTCAGGGTTT CTTTCAGCTT
109851 GAGGGTGATC ATTAACCCTA AAAACTTTTT TCTCTCCTTA CAGGTGGGTG
109901 GAATTAAAGA CAAAGTGCTG GCGGCACACA GAGCGGGACT GAAGCAAGTC
109951 ATTATTCCTC GGAGAAATGA AAAAGACCTT GAGGGAATCC CAGGCAACGT
110001 ACGACAGGAT TTAAGTTTTG TCACAGCAAG CTGCCTGGAT GAGGTTCTTA
110051 ATGCAGCTTT TGATGGTGGC TTTACTGTCA AGACCAGACC TGGTCTGTTA
110101 AATAGCAAAC TGTAGGTCCA AATCTCAATT TTTTAGAATT TTAAGTTATG
110151 AAGTGCTCAA AGGTACTGAC ACAGTTGATT TTATTCACAC CATTAGGGGT
110201 ATGCAAGATG TCCCTGTTTT ATAAACATAA TCACAACAGT AATAAACCTC
110251 AAGTAGTGGC TAGTGTTTAG TATAGAAATA TAAGATGTTG ATTTAGTAAA
110301 CTGATAAAAA TCGAATTCTT GTCTTTTTAG TGGGATCCTT ACTGTCCCTG
110351 GAAAGATATA GCATAGTGGT TCTCAGCACA GTCTCCAGAA CAGAAGCATC
110401 TGTAGTACCT GGTAACTTGT TAGAAATGTA CATTCTCAGG CTCCACAGCA
110451 GGCCGCCTGA ATCAAATCCT GGGAGGTGGG GACAGAAATC TGTGTTTTAA
110501 GAAGCCTTCC AGGTAATTCT GCTGCACACT CAAGTTCAGG AACCACCGGT
110551 ATAGACCATT ACCTTAGTGG ATTTACCTGT AGAGTTTATT GGATCCTGAA
110601 ACCAATCAAT TACTTAGAAC TAGGCAAAGA TGAAAGTATA GCCAACTATT
110651 CTTGGCTATA TATATATATT CAAGTGGGCC GGGCGTGATG GCTCACACCT
110701 GTAATTCCAG CACTTTGGGA GGTCGAGGTA GGCAGATCAC CGAGCCCAAG
110751 AGTTCAAGAC AATCCTGGCC AACGGCGAAA CTCTGTCTCT ACAAAAAATA
110801 TACAGGCGTG TTAGCATGTG CCTGTAATCC CAGCTTCTTG GGAAGCTGAG
110851 GCACAAGAAT TGCCTGAACC CAGGAGGTGG AGGTTGCAGT GAGCTGGGAT
110901 CGCGCCATTG CACTCCAGCC TGGCTGACAG AGCGAGACTG TCTCTAAAAA
110951 AAAAAGACTC AAGTGGACCC TACAATGAAG CCTACACATC CCAATAGAAG
111001 CCCCTTCTTA TGCTGAGGGA AGCAGCCCTC AGAACATGAT AGCTTGTATC
111051 CAGCAGAGTG GCACGTGCTG GCACACCTCA CAGAAGCACC CTGGCCCTGG
111101 ATGCCTGCAA CCTCAGAAGA GTGCAGCTCC CAGAGGGAGG CAGCCATCCA
111151 TCTGGGATGG TCCTAAGCAT GGAATCCTAA CTCCTGATTC CGTCTCCTAT
111201 TTCTTGCTTG GCTACGCCAG TTCCCAAATC TGGTAGATGT CCATGCCCAT
111251 GTGCTCCTGC TGGGACTCAA TTCAGGCTAT GTATGACTAT GAAGTCAGGC
111301 TCATCTGCTT ACTGGCTGTG TGAACTTTTT GTATCTTGGT TTTCTTCATC
111351 CATGAAATCC AAGTAATACT ACCTAATTGT TACTGTGGAG ATTAAGTTCA
111401 AATGCAATGT ATAGTAATAT TAAGCAATTT CTAGTTATTA TTCTAGCCAG
111451 TAATGGACTT CAGAATCTTT TATTACACAA TATAAGAATA TGTATGTAAA
111501 GACATTTTGG AATTTCCTGG ATGAGAAGGA AGTCTGGGCT GGGCATGGTG
111551 GCTCACGCCT GTAACCCTAG CACTTTAGGA AATCGAGGCG AGTGGATCAC
111601 TTAAGCTCAG GAGTTCAAGG CCAGCCTGGG CAACATGGCA AAACCCCATT
111651 TCTACAAAAA ATACAAAAAT TAGCTGGGCA TGGTGGCACC CGCCTGTAGT
111701 CCAGCTACTT GAGGCTGAGA TGGGAGGATG AGGGAGGTCG GGGCTGCAGT
111751 GAGCCAAGAT CACGCCACTG CACTCCAGCA CCCTGGGCGA CAGAGTGAGA
111801 CCCTGTCTCA AAAAAAAAAA AAAAAAAAAG ATTGGGCCAA AATACTGTGA
111851 TAAAATAGCA GGCCTGCTGA TAAAAGTTTA TCTGAATGCA TTGAGAGGAA
111901 AAGTCCAGAC CTAGGACTAG TTATGGCAGT TGGAGAGAAA GAACATCGGG
111951 ATGTTTGAAA ATATGCCATT GACTATCTTA ACTACTGTAA TTTTATCATT

FIGURE 3A-35

112001 TCCAACGTCA TCTAACTGGG GACTAGAACA AACTGTGAAT TCACTTTCAG
112051 CAACCAGAGG GCGCTAATCC ACACCCACAT CGCTCTGCCC TGTTCCACCC
112101 AGCAGGGGCA ACAAGGATAT AACTTGGGGT TC (SEQ ID NO:3)

FEATURES:
Start: 2019
Exon: 2019-2251
Intron: 2252-10218
Exon: 10219-10453
Intron: 10454-14697
Exon: 14698-14829
Intron: 14830-16705
Exon: 16706-16828
Intron: 16829-19511
Exon: 19512-19675
Intron: 19676-20865
Exon: 20866-20960
Intron: 20961-28103
Exon: 28104-28362
Intron: 28363-35632
Exon: 35633-35774
Intron: 35775-54225
Exon: 54226-54376
Intron: 54377-57961
Exon: 57962-58088
Intron: 58089-61472
Exon: 61473-61606
Intron: 61607-92522
Exon: 92523-92665
Intron: 92666-105818
Exon: 105819-106026
Intron: 106027-106411
Exon: 106412-106602
Intron: 106603-109893
Exon: 109894-110112
Stop: 110113

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
12469	T	-	Intron			

Context:

DNA
Position

12469 AACCTTTTCTCTTCACTGAGCCTTTCTAAAAGAAGTCTGGGGCATCCCATTCCCTTGAGT
AAAAGACTTTAATGGCTATAGGATGGACACCAAATTTCTTAGTATAACATTAAGACCGTT
TGCAACTTGTCTTGGGCCTATCTGTCTTGCGTCAACTCTAGTTATCACCTCACTGACACC
CTAGTTCTAGCTCTACTGAATGTAAAACAGCTTCACATTGAGTTATTTTATGTCTCTATG
ATTCTGCCTTCAGTTCTCTGCTGGGAGTGCTCTTCCATCTCTGATTTTTTTTTTTTTTT
[T,-]
GAAATGGAGTCTTGCCCTGTTGCCCAGGCTGGAGTGCAGTGGTGCAATTTCGGCTCACTG
CAGCCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCTTCAGCCTCCCAAGTAGCTGGCAT
TACAGGCATGCGCCACCACGCCCGGCTAACTTTTTGTGTCTTTAGTAGAGATGAGGTTTC
ACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCATGATCCAACCGCCACCACGCCC
GGCCTCCATCTCTGAATTTTAAAATTGAATCTATGCTTTCCCAACAGCTGTAGGCTGTTA

Chromosome map:
Chromosome 16

FIGURE 3A-36